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Tozer, Eileen Collins
Zhang, Feiyu
           Abulencia, Carl
           Frey, Gerhardt
           Parra-Gessert, Lilian
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Gly His Gly Lys Pro Tyr Ala Gly Thr Asn Phe Val Lys Leu Val Val 45
Thr Arg Gly Gly Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Gln 50 60
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Glu Pro Ser Thr Glu Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly
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Ala Phe Lys Thr Ile Tyr Arg Ser Lys Lys Asn Leu Thr Leu Pro Asp
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Cys Leu Tyr Tyr Val Asp Thr Lys Leu Asp Ile Arg Lys Phe Asp Glu
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Thr Lys Gly Gly Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Gln 50 60
Phe Gln Tyr Gly Asn Lys Thr Phe Val Ser Tyr Pro Arg Asp Ile Pro 65 70 75 80
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165 170 175
Ala Phe Lys Thr Ile Tyr Arg Ser Lys Lys Asn Leu Thr Leu Pro Asp
180 185 190
Cys Phe Tyr Tyr Val Asp Thr Lys Leu Asp Ile Arg Lys Phe Asp Glu
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Gly His Gly Lys Pro Tyr Ala Gly Thr Asn Phe Val Lys Leu Val Val
35 40 45
Thr Lys Gly Gly Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Gln 50 55 60
Phe Gln Tyr Gly Asn Lys Thr Phe Val Ser Tyr Pro Arg Asp Ile Pro 65 70 75 80
Asp Tyr Ile Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile
85 90 95
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Asp Ile Asp Lys Thr Leu Lys Leu Ser Gly Gly His Tyr Thr Cys
165 170 175
Ala Phe Lys Thr Ile Tyr Arg Ser Lys Lys Asn Leu Thr Leu Pro Asp
180 185 190
Cys Phe Tyr Tyr Val Asp Thr Lys Leu Asp Ile Arg Lys Phe Asp Glu
195 200 205
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Thr Lys Gly Gly Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Gln 50 60
Leu Gln Tyr Gly Asn Lys Ser Phe Val Ser Tyr Pro Ala Asp Ile Pro 65 70 75 80
Asp Tyr Ile Lys Leu Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile 85 90 95
Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser 100 105 110
                                                 Page 4
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                                                          125
                                  120
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                             135
Glu Pro Ser Thr Glu Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly
145 150 155 160
                                                                        160
Asp Ile His Lys Thr Leu Lys Leu Ser Gly Gly Gly His Tyr Thr Cys
165 170 175
Val Phe Lys Thr Ile Tyr Arg Ser Lys Lys Asn Leu Thr Leu Pro Asp
180 185 190
Cys Phe Tyr Tyr Val Asp Thr Lys Leu Asp Ile Arg Lys Phe Asp Glu
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35 40 45
                                 40
Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala Phe Gln Tyr Gly 50 60
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Asn Arg Thr Phe Thr Lys Tyr Pro Gly Asn Ile Pro Asp Phe Phe Lys 75 75 80
Gln Thr Val Ser Gly Gly Gly Tyr Thr Trp Glu Arg Lys Met Thr Tyr
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Glu Asp Gly Gly Ile Ser Asn Val Arg Ser Asp Ile Ser Val Lys Gly 100 105 110
Asp Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His
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145 150 155 160
Asn Met Ala Leu Leu Lys Asp Gly Arg His Leu Arg Val Asp Phe
165 170 175
                    165
Asn Thr Ser Tyr Ile Pro Lys Lys Val Glu Asn Met Pro Asp Tyr
180 185 190
His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys
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Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala Phe Gln Tyr Gly 50 55 60
Asn Arg Thr Phe Thr Lys Tyr Pro Gly Asn Ile Pro Asp Phe Phe Lys 75 75 80
Gln Thr Val Ser Gly Gly Gly Tyr Thr Trp Glu Arg Lys Met Thr Tyr
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Glu Asp Gly Gly Ile Ser Asn Val Arg Ser Asp Ile Ser Val Lys Gly
100 105 110
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130 135 140
                                                 Page 6
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165 170 175
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Asn Thr Ser Tyr Ile Pro Lys Lys Lys Val Glu Asn Met Pro Asp Tyr
180 185 190
His Phe Ile Asp His Arg Ile Glu Île Leu Gly Asn Pro Glu Asp Lys
195 200 205
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Glu Lys Asn Lys
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Phe Ser Phe Asp Val Leu Thr Pro Ala Phe Gln Tyr Gly Asn Arg Thr 50 60
Phe Thr Lys Tyr Pro Gly Asn Ile Pro Asp Phe Phe Lys Gln Thr Val 65 70 75 80
Ser Gly Gly Gly Tyr Thr Trp Glu Arg Lys Met Thr Tyr Glu Asp Gly 85 90 95
Gly Ile Ser Asn Val Arg Ser Asp Ile Ser Val Lys Gly Asp Ser Phe
100 105 110
Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Ser His Gly Pro Val
Met Gln Lys Lys Thr Val Lys Trp Glu Pro Ser Thr Glu Val Met Tyr
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val Asp Asp Lys Ser Asp Gly Val Leu Lys Gly Asp Val Asn Met Ala
145 150 155 160
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60

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Pro Leu Thr Phe Ser Phe Asp Ile Leu Thr Pro Val Phe Met Tyr Gly 50 60
Asn Arg Ala Phe Thr Lys Tyr Pro Glu Ser Ile Pro Asp Phe Phe Lys 65 70 75 80
Gln Thr Val Ser Gly Gly Gly Tyr Thr Trp Lys Arg Lys Met Ile Tyr
Asp His Glu Ala Glu Gly Val Ser Thr Val Asp Gly Asp Ile Ser Val
                                       105
                                                                110
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Glu Asp Gly Ala Val Met Gln Lys Met Thr Glu Lys Trp Glu Pro Ser
                             135
Thr Glu Val Met Tyr Lys Asp Asp Lys Asn Asp Asp Val Leu Lys Gly
145 150 155 160
                                                                          160
Asp Val Asn His Ala Leu Leu Leu Lys Asp Gly Arg His Val Arg Val
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Asp Phe Asn Thr Ser Tyr Lys Ala Lys Ser Lys Ile Glu Asn Met Pro
180 185 190
Gly Tyr His Phe Val Asp His Arg Ile Glu Ile Ile Gly Arg Ser Ser
195 200 205
Gln Asp Thr Lys Val Lys Leu Phe Glu Asn Ala Val Ala Arg Cys Ser
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Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala Phe Gln Tyr Gly 50 55 60
Asn Arg Thr Phe Thr Lys Tyr Pro Gly Asn Ile Pro Asp Phe Phe Lys 75 75 80
Gln Thr Val Ser Gly Gly Gly Tyr Thr Trp Glu Arg Lys Met Thr Tyr
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Glu Asp Gly Gly Ile Ser Asn Val Arg Ser Asp Ile Ser Val Lys Gly
100 105 110
Asp Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His 115 120 125
Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu
130 135 140
Val Met Tyr Val Asp Asp Lys Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
Asn Met Ala Leu Leu Leu Lys Asp Gly Arg His Leu Arg Val Asp
165 170 175
Asn Thr Ser Tyr Ile Pro Lys Lys Lys Val Glu Asn Met Pro Asp Tyr
180 185 190
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His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys
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Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala Phe Gln Tyr Gly 50 60
Asn Arg Thr Phe Thr Lys Tyr Pro Gly Asn Ile Pro Asp Phe Phe Lys 65 70 75 80
GIn Thr Val Ser Gly Gly Gly Tyr Thr Trp Glu Arg Lys Met Thr Tyr
85 90 95
Glu Asp Gly Gly Ile Ser Asn Val Arg Ser Asp Ile Ser Val Lys Gly
100 105 110
Asp Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His 115 120 125
Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu
130 135 140
Val Met Tyr Val Asp Asp Lys Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
Asn Met Ala Leu Leu Leu Lys Asp Gly Arg His Leu Arg Val Asp Phe
165 170 175
Asn Thr Ser Tyr Ile Pro Lys Lys Val Glu Asn Met Pro Asp Tyr
180 185 190
His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys
                                                     Page 10
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Pro Val Lys Leu Tyr Glu Cys Ala Val Ala Arg Tyr Ser Leu Leu Pro
210 215 220
Glu Lys Asn Lys Ser Lys Gly Asn Ser Lys Leu Glu Gly Lys Pro Ile
225 230 235 240
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                                                                             540
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Ser Phe Ala Asn Gly Ile Ala Glu Glu Met Met Thr Asp Leu His Leu
35 40 45
Glu Gly Ala Val Asn Gly His His Phe Thr Ile Lys Gly Glu Gly Gly 50 55 60
Gly Tyr Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn
65 70 75 80
Gly Ala Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met 85 90 95
Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro His Tyr
100 105 110
Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Ile Pro
115 120 125
Phe Gln Asp Gln Ala Ser Cys Thr Val Thr Ser His Ile Arg Met Lys
Glu Glu Glu Glu Arg His Phe Leu Leu Asn Val Lys Phe Tyr Cys Val
145 150 155 160
Asn Phe Pro Pro Asn Gly Pro Val Met Gln Arg Arg Ile Arg Gly Trp
                                       170
Glu Pro Ser Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly
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Glu Phe Arg Ser Ser Tyr Lys Gly Lys His Ser Ile Asn Met Pro Asp 210 215 220
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                                                                                   300
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Glu Gly Ala Val Asn Gly His His Phe Thr Ile Lys Gly Glu Gly Gly 50 55 60
Gly Tyr Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn 65 70 80
Gly Ala Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met 85 90 95
Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr
100 105 110
Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Ile Pro
115 120 125
Phe Gln Asp Gln Ala Ser Cys Thr Val Thr Ser His Ile Arg Met Lys
130 135 140
Glu Glu Glu Glu Arg His Phe Leu Leu Asn Val Lys Phe Tyr Cys Val
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Glu Pro Ser Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly
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195 200 205
Glu Phe Arg Ser Ser Tyr Lys Gly Lys His Ser Ile Asn Met Pro Asp
210 215 220
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Leu Pro Ser Val His
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Gly Ala Val Asn Gly His His Phe Thr Ile Lys Gly Glu Gly Gly Gly 50
Tyr Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly 65
70
75
80
Ala Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr
85 90 95
Gly Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe 100 105 110
Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Ile Pro Phe
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Gln Asp Gln Ala Ser Cys Thr Val Thr Ser His Ile Arg Met Lys Glu
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165 170 175
Pro Ser Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly His
180 185 190
Asp Asp Met Thr Leu Arg Val Glu Gly Gly Gly Tyr Tyr Arg Ala Glu
195 200 205
        Ser Ser Tyr Lys Gly Lys His Ser Ile Asn Met Pro Asp Phe
   Phe Ile Asp His Arg Ile Glu Ile Met Glu His Asp Glu Asp 230 235
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Thr Lys Gly Gly Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Gln 50 60
Leu Gln Tyr Gly Asn Lys Ser Phe Val Ser Tyr Pro Ala Asp Ile Pro
65 70 75 80
Asp Tyr Ile Lys Leu Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile
Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser
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                                   120
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Asp Ile His Lys Thr Leu Lys Leu Ser Gly Gly His Tyr Thr Cys
165 170 175
Val Phe Lys Thr Ile Tyr Arg Ser Lys Lys Asn Leu Thr Leu Pro Asp
180 185 190
Cys Phe Tyr Tyr Val Asp Thr Lys Leu Asp Ile Arg Lys Phe Asp Glu
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Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala Phe Gln Tyr Gly 50 55
Asn Arg Thr Phe Thr Lys Tyr Pro Gly Asn Ile Pro Asp Phe Phe Lys 75 80
Gin Thr Val Ser Gly Gly Gly Tyr Thr Trp Glu Arg Lys Met Thr Tyr
85 90 95
Glu Asp Gly Gly Ile Ser Asn Val Arg Ser Asp Ile Ser Val Lys Gly
Asp Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His
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130 135 140
 val Met Tyr Val Asp Asp Lys Ser Asp Gly Val Leu Lys Gly Asp Val 145 _ 150 _ 160
 Asn Met Ala Leu Leu Leu Lys Asp Gly Arg His Leu Arg Val Asp Phe 165 170 175
 Asn Thr Ser Tyr Ile Pro Lys Lys Lys Val Glu Asn Met Pro Asp Tyr 180 185 190
 His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys
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200
205
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35 40 45
Glu Gly Ala Val Asn Gly His His Phe Thr Ile Lys Gly Glu Gly Gly 50 _ _ _ 55 _ _ 60 _ _ _ _ 7
Gly Tyr Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn 70 75 80
Gly Ala Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met
85_ 90 95
Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr
Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Ile Pro
                                              Page 16
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130 135 140
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                        150
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Asn Phe Pro Pro Asn Gly Pro Val Met Gln Arg Arg Ile Arg Gly Trp
165 170 175
Glu Pro Ser Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly
                                      185
              180
His Asp Asp Met Thr Leu Arg Val Glu Gly Gly Gly Tyr Tyr Arg Ala
195 200 205
Glu Phe Arg Ser Ser Tyr Lys Gly Lys His Ser Ile Asn Met Pro Asp 210 215 220
Phe His Phe Ile Asp His Arg Ile Glu Ile Met Glu His Asp Glu Asp
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Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 _ _ _ 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
GÎn Thr Phe Pro Glu GÎy Tyr His Trp Glu Arg Lys Met Thr Tyr Glu
85 90 95
                                              Page 17
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Leu Leu Lys Asp Gly Gly His Tyr Thr Cys Val Phe Lys Thr Ile Tyr 165 - 170 175
Arg Ser Lys Lys Val Glu Asn Met Pro Asp Tyr His Phe Ile Asp
180 185 190
His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn His Val Lys
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 Val Asn Gly Ala Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Ala
50 55 60
 Phe Met Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro 65 70 75 80
 Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile
                                                 Page 18
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Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser
Val Lys Gly Asp Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn 115 120 125
Phe Pro Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu
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Pro Ser Thr Glu Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly His 155 160
Asp Asp Met Thr Leu Arg Val Glu Gly Gly Gly His Tyr Thr Cys Val
165 170 175
Phe Lys Thr Ile Tyr Arg Ser Lys Lys Lys Val Glu Asn Met Pro Asp
180 185 190
Tyr His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asm Pro Glu Asp
195 200 205
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35 40 45
Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala Phe Met Tyr Gly 50 55 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe 65 70 75
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Ile Pro Phe Gln
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120
125
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Met Ala Leu Leu Lys Asp Gly Gly Tyr Tyr Arg Ala Glu Phe Arg
165 170 175
Ser Ser Tyr Lys Gly Lys His Ser Ile Asn Met Pro Asp Phe His Phe 180 185 190
Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val
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Val Asn Gly Ala Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Ala 50 55 60
Phe Met Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro 65 70 75 80
Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile
85 90 95
                                                    Page 20
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Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser
100 105 110
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                              135
                                                       140
Pro Ser Thr Glu Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly His
145 150 160
                         150
Asp Asp Met Thr Leu Arg Val Glu Gly Gly Gly His Tyr Thr Cys Val
165 170 175
                   165
Phe Lys Thr Ile Tyr Arg Ser Lys Lys Lys Val Glu Asn Met Pro Asp
180 185 190
         Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp
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Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Gln Leu Gln Tyr Gly 50 55 60
Asn Lys Ser Phe Val Ser Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Ile Pro Phe Gln
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Asp Gln Ala Ser Cys Thr Val Thr Ser Asp Ile Ser Met Lys Ser Asn 100 105 110
Asn Cys Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His 115 120 125
Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu
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Val Met Tyr Val Asp Asp Lys Ser Asp Gly Val Leu Lys Gly His Asp 145 150 155 160
Asp Met Thr Leu Arg Val Glu Gly Gly Arg His Leu Arg Val Asp Phe
165 170 175
Asn Thr Ser Tyr Ile Pro Lys His Ser Ile Asn Met Pro Asp Phe His
180 185 190
Phe Ile Asp His Arg Ile Asp Ile Arg Lys Phe Asp Glu Asn Tyr Ile
195 200 205
Asn Val Glu Gln Asp Glu Ile Ala Thr Ala Arg His His Gly Leu Lys
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Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala Phe Met Tyr Gly 50 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Ile Pro Phe Gln
                                              Page 22
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90
Asp Gln Ala Ser Cys Thr Val Thr Ser Asp Ile Ser Met Lys Ser Asn
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His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr
Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val Asn Met
145 150 160
Ala Leu Leu Leu Lys Asp Gly Arg His Leu Arg Val Asp Phe Asn Thr
165 170 175
Ser Tyr Ile Pro Lys His Ser Ile Asn Met Pro Asp Phe His Phe Ile
                                       185
Asp His Arg Ile Asp Ile Arg Lys Phe Asp Glu Asn Tyr Ile Asn Val
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35 40 45
Lys Glu Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Gln 50 60 ____
    GÎN Tyr Gly Asn Lys Ser Phe Val Ser Tyr Pro Ala Asp Ile
70 75
Asp Tyr Ile Lys Leu Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ser
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115 120 125
Phe Pro Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu
130 135 140
Pro Ser Thr Glu Val Met Tyr Val Asp Asp Lys Ser Asp Gly Val Leu
145 150 160
Lys Gly Asp Val Asn Met Ala Leu Leu Leu Lys Asp Gly Arg His Leu
165 170 175
Arg Val Asp Phe Asn Thr Ser Tyr Ile Pro Lys Lys Lys Val Glu Asn 180 185 190
Met Pro Asp Tyr His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn 195 200 205
Pro Glu Asp Lys Pro Val Lys Leu Tyr Glu Ile Ala Thr Ala Arg His 210 215 220
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Lys Glu Glu Glu Glu Arg His Phe Phe Tyr Asp Ile Lys Phe Thr Gly
Met Asn Phe Pro Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys
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                        150
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165 170 175
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35 40 45
Asp Cys Thr Val Asn Gly Asp Lys Phe Glu Ile Glu Gly Glu Gly Asn 50 55 60
Gly Lys Pro Tyr Ala Gly Val Gln Phe Met Ser Leu Glu Val Val Asn
65 70 75 80
Gly Ala Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Gln Leu Gln
Tyr Gly Asn Lys Ser Phe Val Ser Tyr Pro Lys Glu Ile Pro Asp Tyr
Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Ile Pro
115 120 125
Phe Gln Asp Gln Ala Ser Cys Thr Val Thr Ser Asp Ile Ser Val Lys
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130
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     Phe Asn Thr Ser Tyr Ile Pro Lys His Ser Ile Asn Met Pro Asp 210 220
Phe His Phe Ile Asp His Arg Ile Glu Ile Met Glu His Asp Glu Asp
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Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala Phe Gln Tyr Gly 50 _ _ _ 60
Asn Arg Thr Phe Thr Lys Tyr Pro Ala Asp Ile Pro Asp Tyr Ile Lys 65 70 75 80
Leu Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ser Ile Pro Phe Gln
85 90 95
Asp Gln Ala Ser Cys Thr Val Thr Ser Asp Ile Ser Val Lys Gly Asp
                                                  Page 26
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105
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Gly Pro Val Met Gln Arg Arg Ile Arg Gly Trp Glu Pro Ser Thr Glu
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Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly His Asp Asp Met Thr
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Leu Arg Val Glu Gly Gly Gly Tyr Tyr Arg Ala Glu Phe Arg Ser Ser
165 170 175
Tyr Lys Gly Lys Lys Lys Val Glu Asn Met Pro Asp Tyr His Phe Ile
180 185 190
Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val Lys
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Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp
100 105 110
Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe Pro Pro His
                                                Page 27
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Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu
130 135 140
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Lys Thr Ile Tyr Arg Ser Lys Lys Lys Val Glu Asn Met Pro Asp Tyr
180 185 190
His Phe Ile Asp His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr 195 200 205
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Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Ala Phe Met Tyr Gly 50 55 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
GÎN Thr Phe Pro Glu GÎy Tyr His Trp Glu Arg Ser Ile Pro Phe GÎN
85 90 _ 95
Asp Gln Ala Ser Cys Thr Val Thr Ser Asp Ile Ser Val Lys Gly Asp 100 105 110

Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His Gly 120 125
Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu Arg
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165 170 175
Ile Pro Lys His Ser Ile Asn Met Pro Asp Phe His Phe Ile Asp His
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Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val Lys Leu Tyr
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Thr Lys Gly Gly Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala 50 55 60
Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Ala Asp Ile Pro 65 70 75 80
Asp Tyr Ile Lys Leu Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ser
85 90 95
Ile Pro Phe Gln Asp Gln Ala Ser Cys Thr Val Thr Ser His Ile Arg
100 105 110
Met Lys Glu Glu Glu Arg His Phe Tyr Tyr Lys Ile His Phe Thr
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Gly Glu Phe Pro Pro Asn Gly Pro Val Met Gln Arg Arg Ile Arg Gly 130 135 140
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Val Asp Phe Asn Thr Ser Tyr Ile Pro Lys His Ser Ile Asn Met Pro
                                        185
    Phe His Phe Ile Asp His Arg Ile Glu Ile Met Glu His Asp Glu
195 200 205
    Tyr Asn His Val Lys Leu Arg Glu Ile Ala Thr Ala Arg His His 210 225 220
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35 40 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 60
Asn Arg Val Phe Thr Lys Tyr Pro Gly Asn Ile Pro Asp Phe Phe Lys 65 70 75 80
Gin Thr Val Ser Gly Gly Gly Tyr Thr Trp Glu Arg Ile Met Thr Phe
85_ 90 95
Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly
100 105 110
Asp Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe Pro Pro 115 120 125
His Gly Pro Val Met Gln Arg Lys Thr Val Lys
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                                                      Trp Glu Pro Ser Thr
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Glu Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly His Asp Asp Met
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Thr Leu Arg Val Glu Gly Gly His Tyr Thr Cys Val
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Ile Tyr Arg Ser Lys His Ser Ile Asn Met Pro Asp Phe His Phe Ile
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                                     185
Asp His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn His Val
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                                                        205
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    Leu Arg Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly Lys
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                                                   220
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Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala
35 40 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
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Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp 100 105 110
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Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His Gly
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                                 120
                                                        125
Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu Val
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Met Tyr Val Asp Asp Lys Ser Asp Gly Val Leu Lys Gly Asp Val 145 150 155
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Met Ala Leu Leu Leu Lys Asp Gly Gly His Tyr Thr Cys val Phe Lys
                   165
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 Thr Ile Tyr Arg Ser Lys His Ser Ile Asn Met Pro Asp Phe His Phe
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                                      185
                                                             190
Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val
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                                 200
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Gly Gly Gly Tyr Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val
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                                                        45
Val Asn Gly Ala Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Gln
Leu Gln Tyr Gly Asn Lys Ser Phe Val Ser Tyr Pro Lys Glu Ile Pro 65 70 75 80
Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile
85 90 95
Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser 100 105 110
Val Lys Gly Asp Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe 115 120 125
                                                        125
Pro Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro
                            135
                                                   140
Ser Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val
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                                              155
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Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
85 90 95
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp
100 105 110
Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His Gly 115 120 125
                                                          125
Pro val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu Asn
Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val Asn Met Ala Leu
145 _____150 ____155 ____160
Leu Leu Lys Asp Gly Arg His Leu Arg Val Asp Phe Asn Thr Ser Tyr
165 170 175
Ile Pro Lys Lys Lys Val Glu Asn Met Pro Asp Tyr His Phe Ile Asp
180 185 190
His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val Lys Leu
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Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala
Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Gln Leu Gln Tyr Gly 50 60
Asn Lys Ser Phe Val Ser Tyr Pro Gly Asn Ile Pro Asp Phe Phe Lys 65 70 75 80
Gln Thr Val Ser Gly Gly Gly Tyr Thr Tyr Tyr Lys Ile His Phe Thr
85 _____ 90 ___ 95
Gly Glu Phe Pro Pro Asn Gly Pro Val Met Gln Arg Arg Ile Arg Gly
               100
                                         105
Trp Glu Pro Ser Thr Glu Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr
115 120 125
Gly Asp Ile His Lys Thr Leu Lys Leu Ser Gly Gly Arg His Leu Arg
     130
                              135
Val Asp Phe Asn Thr Ser Tyr Ile Pro Lys His Ser Ile Asn Met Pro
                         150
                                                   155
Asp Phe His Phe Ile Asp His Arg Ile Asp Ile Arg Lys Phe Asp Glu
165 170 175
Asn Tyr Ile Asn Val Glu Gln Asp Glu Ile Ala Thr Ala Arg His His 180 185 190
Gly Leu Lys Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser
Thr Arg Thr Gly
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420

480

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Gly Asn Gly Lys Pro Tyr Ala Gly Thr Asn Phe Val Lys Leu Val Val
35 40 45
Thr Lys Gly Gly Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala 50 55 60
Phe Met Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro 65 70 75 80
Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile
85 90 95
Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser
100 105 110
Val Lys Gly Asp Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn 115 120 125
Phe Pro Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu
130 135 140
Pro Ser Thr Glu Val Met Tyr Val Asp Asp Lys Ser Asp Gly Val Leu 145 _ _ _ _ 160
Lys Gly Asp Val Asn Met Ala Leu Leu Leu Lys Asp Gly Gly Tyr Tyr
165 170 175
Arg Ala Glu Phe Arg Ser Ser Tyr Lys Gly Lys Lys Lys Val Glu Asn
180 185 190
Met Pro Asp Tyr His Phe Ile Asp His Arg Ile Glu Ile Met Glu His
195 200 205
Asp Glu Asp Tyr Asn His Val Lys Leu Arg Glu Ile Ala Thr Ala Arg
                               215
                                                         220
His His Gly Leu Lys Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu
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Asp Ser Thr Arg Thr Gly
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360 420 480

540 600

660 720

741

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                                                                                               240
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                                                                                               300
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                                                                                               420
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Met Ser Leu Glu Val Val Asn Gly Ala Pro Leu Pro Phe Ser Phe Asp 35 40 45
Ile Leu Thr Pro Gln Leu Gln Tyr Gly Asn Lys Ser Phe Val Ser Tyr
Pro Lys Glu Ile Pro Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr 65 70 75 80
His Trp Glu Arg Ile Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile
85 90 95
Thr Ser Asp Ile Ser Val Lys Gly Asp Ser Phe Tyr Tyr Lys Ile His 100 105 110
Phe Thr Gly Glu Phe Pro Pro His Gly Pro Val Met Gln Arg Lys Thr
Val Lys Trp Glu Pro Ser Thr Glu Val Met Tyr Val Asp Asp Lys Ser
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Asp Gly Val Arg Arg Asp Met Thr Thr
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cagacctttc ctgaaggcta tcactgggag cgaataatga cttttgagga cgggggcgta
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                                                                                              480
                                                                                              540
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Pro Tyr Ala Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala 35 40 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
Asp Gly Gly Val Cys Cys Ile Thr Ser His Ile Arg Met Lys Glu Glu
100 105 110
Glu Glu Arg His Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro
115 120 125
Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser
     130
                            135
                                                   140
Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val Asn
                                              155
                       150
                                                                     160
Met Ala Leu Leu Leu Lys Asp Gly Arg His Leu Arg Val Asp Phe Asn
                  165
                                          170
Thr Ser Tyr Ile Pro Lys Lys Lys Val Glu Asn Met Pro Asp Tyr His
180
185
190
Phe Ile Asp His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn
195 200
His Val Lys Leu Arg Glu Ile Ala Thr Ala Arg His His Gly Leu Lys
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    210
                                                   220
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cactgggagc gaataatgac ttttgaggac gggggcgtat gitgcatcac aagcgacatc
                                                                                 300
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                                                                                 420
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Leu His Leu Thr Glu Lys Glu Gly Lys Pro Leu Pro Phe Gly Trp His 35 40 45
Ile Leu Ser Pro Gln Leu Gln Tyr Gly Asn Lys Ser Phe Val Ser Tyr 50 60
Pro Lys Glu Ile Pro Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr 65 75 80
His Trp Glu Arg Ile Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile
Thr Ser Asp Ile Ser Val Lys Gly Asp Ser Phe Phe Tyr Asp Ile Lys 100 105 110
Phe Thr Gly Met Asn Phe Pro Pro His Gly Pro Val Met Gln Arg Lys
Thr Val Lys Trp Glu Pro Ser Thr Glu Asn Ile Tyr Pro Arg Asp Glu
130 135 140
Phe Leu Glu Gly His Asp Asp Met Thr Leu Arg Val Lys Trp Pro Pro 145 150 155 160
Phe Glu Ser
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Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala
                                               Page 38
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<220>

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85
                                                 90
 Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp
100 105 110
 Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe Pro Pro His
                                      120
      Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu
130 140
     Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly His Asp Asp Met
150 155
Leu Arg Val Glu Gly Gly His Tyr Thr Cys Val Phe Lys Thr Ile
165 170 175
                                                 170
Tyr Arg Ser Lys Lys Lys Val Glu Asn Met Pro Asp Tyr His Phe Ile
180 185 190
Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val Lys 200 205
     Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly Lys Pro 210 220
The Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
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                                                                                              360
                                                                                             420
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Pro Tyr Glu Gly Thr Asn Phe Val Lys Leu Val Val Thr Lys Gly Gly
                                                   Page 39
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Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Gln Leu Gln Tyr Gly 50 60
Asn Lys Ser Phe Val Ser Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Lys Met Thr Tyr Glu
90 95
                                             90
Asp Gly Gly Ile Ser Asn Val Arg Ser His Ile Arg Met Lys Glu Glu 100 105 110
Glu Glu Arg His Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe
115 120 125
    Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro 130 135 140
Ser Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly His Asp
145 150 155
Asp Met Thr Leu Arg Val Glu Gly Gly Gly His Tyr Thr Cys Val Phe 165 170 175
Lys Thr Ile Tyr Arg Ser Lys His Ser Ile Asn Met Pro Asp Phe His
180 185 190
Phe Ile Asp His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn 195 200 205
    Val Lys Leu Arg Glu Ile Ala Thr Ala Arg His His Gly Leu Lys
                              215
Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg
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20 25 30
Gly Asn Gly Lys Pro Tyr Ala Gly Val Gln Phe Met Ser Leu Glu Val
                                                Page 40
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Val Asn Gly Ala Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala
                                55
Phe Met Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro 65 70 75 80
Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile
85 90 95
Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser
100 105 110
Val Lys Gly Asp Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn
115 120 125
Phe Pro Pro Asn Gly Pro Val Met Gln Arg Arg Ile Arg Gly Trp Glu
130 135 140
Pro Ser Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly His
145 150 160
Asp Asp Met Thr Leu Arg Val Glu Gly Gly Gly His Tyr Thr Cys Val
165 170 175
Phe Lys Thr Ile Tyr Arg Ser Lys His Ser Ile Asn Met Pro Asp Phe 180 185 190
His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys
           195
                                      200
                                                                 205
Pro Val Lys Leu Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu Lys 210 215 220
Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr 225 230 235 240
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                                                                                               240
cagacettic etgaaggeta teaetgggag egaataatga ettttgagga egggggegta
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tgttgcatca caagcgacat cagtgtgaaa ggtgactctt tctactataa gattcacttc actggcgagt ttcctcctca tggtccagtg atgcagagaa agacagtaaa atgggagcca tccactgaaa acatttatcc tcgcgacgaa tttctggagg gacatgacga catgactctg
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                                                                                               717
<210> 84
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Met Lys Gly Val Lys Glu Val Met Lys Ile Ser Leu Glu Met Asp Cys

1 10 15
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Pro Tyr Ala Gly Thr Asn Phe Val Lys Leu Val Val Thr Lys Gly Gly
                                                    Page 41
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Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Gln Leu Gln Tyr Gly 50 55 60
Asn Lys Ser Phe Val Ser Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
                                           90
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp
Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His Gly 115 120 125
Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu Asn
130 135 140
Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly His Asp Asp Met Thr
                                                155
                        150
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Arg Val Glu Gly Gly Tyr Tyr Arg Ala Glu Phe Arg Ser Ser Tyr
                   165
                                           170
                                                                   175
Lys Gly Lys Lys Asn Leu Thr Leu Pro Asp Cys Phe Tyr Tyr Val Asp
180 185 190
Thr Lys Leu Glu Ile Met Glu His Asp Glu Asp Tyr Asn His Val Lys
195 200 205
Leu Arg Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly Lys Pro
210 215 220
Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
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                                                                                    300
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35 40 45
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Ser Asp Ile Ser Met Lys Ser Asn Asn Cys Phe Tyr Tyr Lys Ile His 50 55 60
Phe Thr Gly Glu Phe Pro Pro Asn Gly Pro Val Met Gln Arg Arg Ile
                                              Page 42
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Tyr Arg Ala Glu Phe Arg Ser Ser Tyr Lys Gly Lys His Ser Ile Asn
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                                 120
Met Pro Asp Phe His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn
     130
                            135
Pro Glu Asp Lys Pro Val Lys Leu Tyr Glu Ile Ala Thr Ala Arg His
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Ser Thr Arg Thr Gly
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35 40 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 55 60
Asn Arg Val Phe Thr Lys Tyr Pro Ala Asp Ile Pro Asp Tyr Ile Lys 65 70 75 80
Leu Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Thr Phe Glu
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Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp 100 - 105 - 110
Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe Pro Pro His 115 120 125
Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu
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Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val Asn Met Ala
145 150 155 160
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Tyr Arg Ser Lys His Ser Ile Asn Met Pro Asp Phe His Phe Ile Asp
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His Arg Ile Asp Ile Arg Lys Phe Asp Glu Asn Tyr Ile Asn Val Glu
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35 40 45
Val Asn Gly Ala Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala 50 55 60
Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Lys Glu Ile Pro 65 70 75 80
Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Lys
85 90 _ 95
Met Thr Tyr Glu Asp Gly Gly Ile Ser Asn Val Arg Ser Asp Ile Ser 100 105 110
Val Lys Gly Asp Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn
115 120 125
Phe Pro Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu
130 135 140
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Pro Ser Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp
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                                               170
 Phe Asn Thr Ser Tyr Ile Pro Lys Lys Lys Val Glu Asn Met Pro Asp
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 Tyr His Phe Ile Asp His Arg Ile Glu Ile Met Glu His Asp Glu Asp
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Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Gln Leu Gln Tyr Gly 50 60
Asn Lys Ser Phe Val Ser Tyr Pro Ala Asp Ile Pro Asp Tyr Ile Lys 70 75 80
Leu Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ile Met Thr Phe Glu
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                                             90
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp 100 105 110
Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His Gly
115 120
                                   120
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Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu Val
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Thr Ile Tyr Arg Ser Lys Lys Lys Val Glu Asn Met Pro Asp Tyr His
180 185 190
Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro 195 200 205
Val Lys Leu Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly 210 215 220
Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly 225 230 235 240
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Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 ____ 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
GÎN Thr Phe Pro Glu GÎy Tyr His Trp Glu Arg Lys Met Thr Tyr Glu
85 90 _ 95 _
Asp Gly Gly Ile Ser Asn Val Arg Ser His Ile Arg Met Lys Glu Glu 100 105 110
Glu Glu Arg His Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro
115 120 125
Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser
130 135 140
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Thr Glu Val Met Tyr Val Asp Asp Lys Ser Asp Gly Val Leu Lys Gly
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145
Asp Val Asn Met Ala Leu Leu Leu Lys Asp Gly Arg His Leu Arg Val
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180 185 190
Asp Tyr His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu
195 200 205
        Pro Val Lys Leu Tyr Glu Ile Ala Thr Ala Arg His His Gly 215 220
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Arg Thr Gly
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Val Asn Gly Ala Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala
Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Lys Glu Ile Pro 65 70 75 80
Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile
85 90 95
Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser 100 105 110
         Ser Asn Asn Cys Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu
Phe Pro Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu
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Pro Ser Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp
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Phe Asn Thr Ser Tyr Ile Pro Lys Lys Val Glu Asn Met Pro Asp
Tyr His Phe Ile Asp His Arg Ile Glu Ile Met Glu His Asp Glu Asp 195 200 205
Tyr Asn His Val Lys Leu Arg Glu Cys Ala Val Ala Arg Tyr Ser Leu
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35 40 45
Glu Glu Glu Arg His Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu
50 55 60
Phe Pro Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu 65 70 75 80
Pro Ser Thr Glu Val Met Tyr Val Asp Asp Lys Ser Asp Gly Val Leu
85 90 95
Lys Gly His Asp Asp Met Thr Leu Arg Val Glu Gly Gly Gly Tyr Tyr
Arg Ala Glu Phe Arg Ser Ser Tyr Lys Gly Lys Lys Lys Val Glu Asn
Met Pro Asp Tyr His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn 130 135 140
Pro Glu Asp Lys Pro Val Lys Leu Tyr Glu Cys Ala Val Ala Arg Tyr
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Gly Thr Asn Phe Val Lys Leu Val Val Thr Lys Gly Gly Pro Leu Thr
Phe Ser Phe Asp Val Leu Thr Pro Gln Leu Gln Tyr Gly Asn Lys Ser 50 60
Phe Val Ser Tyr Pro Ala Asp Ile Pro Asp Tyr Ile Lys Leu Ser Phe 65 70 75 80
Pro Glu Gly Phe Thr Trp Glu Arg Ser Ile Pro Phe Gln Asp Gln Ala
Ser Cys Thr Val Thr Ser Asp Ile Ser Val Lys Gly Asp Ser Phe Tyr
100 105 110
Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His Gly Pro Val Met
115 120 125
Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu Arg Leu Tyr Leu
130 135 140
Arg Asp Gly Val Leu Thr Gly His Asp Asp Met Thr Leu Arg Val Glu
145 150 155 160
Gly Gly Arg His Leu Arg Val Asp Phe Asn Thr Ser Tyr Ile Pro Lys
                                            170
                   165
Lys Asn Leu Thr Leu Pro Asp Cys Phe Tyr Tyr Val Asp Thr Lys Leu
                                       185
Asp Ile Arg Lys Phe Asp Glu Asn Tyr Ile Asn Val Glu Gln Asp Glu
195 200 205
Cys Ala Val Ala Arg Tyr Ser Leu Leu Pro Glu Lys Asn Lys Gly Lys
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215
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Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala
35 40 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 _ _ _ 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gin Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
85 90 95
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp
100 105 110
Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe Pro Pro His
Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu
130 135 140
Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val Asn Met Ala
145 150 160
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Leu Leu Leu Lys Asp Gly Gly Tyr Tyr Arg Ala Glu Phe Arg Ser Ser
165 170 175
Tyr Lys Gly Lys His Ser Ile Asn Met Pro Asp Phe His Phe Ile Asp
                                        185
                                                                190
His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val Lys Leu
195 200 205
                                                           205
                                                      Lys Gly Lys Pro Ile
220
Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu
210 215
Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
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<211> 238 <212> PRT <213> Artificial Sequence

<220> <223> Synthetically generated

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60

120

180

240 300

360 420 480

540 600

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                                                                                       120
                                                                                       180
ttacagtatg gaaacaagtc attcgtcagc tacccagccg atataccaga ctatatcaag
                                                                                       240
ctgtcčtttč čtgagggčtt taccigggāg cgaagcāttč cttttcaaga ccaggcctcă
                                                                                       300
tgtaccgtca caagccacat caggatgaaa gaggaagagg agcggcattt ctactataag attcacttca ctggcgagtt tcctcctaat ggtccagtga tgcagaggag gatacgagga
                                                                                       360
                                                                                       420
tgggagccat ccactgaaaa catttatcct cgcgacgaat tictggaggg agataiccac
                                                                                       480
aagactctga aacttagcgg tggccgccat ttgagagttg actttaacac ttcttacata
                                                                                       540
cccaagcact cgatcaacat gccggatttc cattttatag accaccgcat tgatattcgg
aagttcgacg aaaattacat caacgtcgag caggacgaga ttgctacagc tcgccatcat
gggctgaagg gtaagcctat ccctaaccct ctcctcggac tcgattctac gcgtaccggt
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                                                                                       723
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Pro Tyr Glu Gly Thr Gln Thr Leu His Leu Thr Glu Lys Glu Gly Lys 35 40 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Gln Leu Gln Tyr Gly 50 60
Asn Lys Ser Phe Val Ser Tyr Pro Ala Asp Ile Pro Asp Tyr Ile Lys 65 70 75 80
Leu Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ser Ile Pro Phe Gln
                                            90
Asp Gln Ala Ser Cys Thr Val Thr Ser His Ile Arg Met Lys Glu Glu
100 105 110
Glu Glu Arg His Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro
115 120 125
Pro Asn Gly Pro Val Met Gln Arg Arg Ile Arg Gly Trp Glu Pro Ser
130 140
                             135
Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Ile His
                        150
                                                 155
Lys Thr Leu Lys Leu Ser Gly Gly Arg His Leu Arg Val Asp Phe Asn
                   165
                                            170
Thr Ser Tyr Ile Pro Lys His Ser Ile Asn Met Pro Asp Phe His Phe 180 190
                                                                190
Ile Asp His Arg Ile Asp Ile Arg Lys Phe Asp Glu Asn Tyr Ile Asn 195 200 205
Val Glu Gln Asp Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly
210 215 220
Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
225 230 235
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<210> 107

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                                                                                         120
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tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag
cagacctttc ctgaaggcta tcactgggag cgaataatga cttttgagga cgggggcgta
                                                                                         180
                                                                                         240
                                                                                         300
tgttgcatca caagccacat caggatgaaa gaggaagagg agcggcatit ctactataag
                                                                                         360
                                                                                         420
attcacttca ctggcgagtt tcctcctaat ggtccagtga tgcagaggag gatacgagga
tgggagccat ccactgaaaa catttatcct cgcgacgaat ttctggaggg acatgacgac atgactctgc gggttgaagg tggcggctat tacagagctg aatttagaag ttcttacaaa ggcaagcact cgatcaacat gccggatttc cattttatag accaccgcat tgagattctg
                                                                                         480
                                                                                         540
                                                                                         600
ggcaacccag aagacaagcc ggtcaagctg tacgagattg ctacagctcg ccatcatggg
                                                                                         660
ctgaagggta agcctatccc taaccctctc ctcggactcg attctacgcg taccggttag
                                                                                         720
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<211> 239
<212> PRT
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20 25 30
Pro Tyr Glu Gly Thr Gln Thr Leu His Leu Thr Glu Lys Glu Gly Lys
35 40 45
Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala Phe Met Tyr Gly 50 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
GĪn Thr Phe Pro Glu GĪy Tyr His Trp Glu Arg Ile Met Thr Phe Glu
85 90 95
Asp Gly Gly Val Cys Cys Ile Thr Ser His Ile Arg Met Lys Glu Glu
100 105 110
Glu Glu Arg His Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro
115 120 125
Pro Asn Gly Pro Val Met Gln Arg Arg Ile Arg Gly Trp Glu Pro Ser
Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly His Asp Asp 145 150 155 160
                                                  155
Met Thr Leu Arg Val Glu Gly Gly Gly Tyr Tyr Arg Ala Glu Phe Arg
165 170 175
Ser Ser Tyr Lys Gly Lys His Ser Ile Asn Met Pro Asp Phe His Phe 180 190
Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val
195 200 205
Lys Leu Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly Lys 210 215 _ 220
Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly 225 230 235
225
                         230
<210> 109
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                                                                                              120
                                                                                              180
                                                                                              240
                                                                                              300
gacgggggcg tatgttgcat cacaagcgac atcagtgtga aaggtgactc tttcttctat gacattaagt tcactggcat gaactttcct cctaatggtc cagtgatgca gaggaggata cgaggatggg agccatccac tgaagtaatg tatgttgacg acaagagtga cggtgtgctg
                                                                                              360
                                                                                              420
                                                                                              480
aagggacatg acgacatgac tctgcgggtt gaaggtggcg gccattacac atgtgtcttt
                                                                                              540
                                                                                              600
aaaactattt acagatccaa gcactcgatc aacatgccgg atttccattt tatagaccac
cgcattgaga ttctgggcaa cccagaagac aagccggtca agctgtacga gtgtgctgta gctcgctatt ctctgctgcc tgagaagaac aagggtaagc ctatccctaa ccctctcctc
                                                                                              660
                                                                                              720
ggactcgatt ctacgcgtac cggttag
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<211> 248
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<213> Artificial Sequence
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His Leu Glu Gly Thr Phe Asn Gly His Lys Phe Thr Ile Lys Gly Glu
20 25 30
Gly Gly Gly Tyr Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val
35 40 45
Val Asn Gly Ala Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Ala 50 55 60
Phe Met Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro 65 70 75 80
Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile
85 90 95
Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser 100 105 110
Val Lys Gly Asp Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn
115 120 125
Phe Pro Pro Asn Gly Pro Val Met Gln Arg Arg Ile Arg Gly Trp Glu
130 135 140
Pro Ser Thr Glu Val Met Tyr Val Asp Asp Lys Ser Asp Gly Val Leu
145 150 155 160
Lys Gly His Asp Asp Met Thr Leu Arg Val Glu Gly Gly His Tyr
                                                170
                     165
Thr Cys Val Phe Lys Thr Ile Tyr Arg Ser Lys His Ser Ile Asn Met
                                          185
Pro Asp Phe His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro
                                     200
                                                                205
Glu Asp Lys Pro Val Lys Leu Tyr Glu Cys Ala Val Ālā Arg Tyr Ser
210 215 220
Leu Leu Pro Glu Lys Asn Lys Gly Lys Pro Ile Pro Asn Pro Leu Leu
225 230 235 240
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Gly Leu Asp Ser Thr Arg Thr Gly
<210> 111
<211> 561
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 <223> Synthetically generated
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                                                                                                60
                                                                                               120
gacgggggcg tatgitgcat cacaagcgac atcagtgiga aaggtgactc ittctaciai aagattcact tcactggcga gtttcctcct aatggtccag tgatgcagag gaggatacga
                                                                                               180
                                                                                               240
ggatgggagc catccactga aaacatttat cctcgcgacg aatttctgga gggacatgac
                                                                                               300
gacatgactc tgcgggttga aggtggcggc cattacacat gtgtctttaa aactatttac
                                                                                               360
agatccaaga agaaggtcga gaatatgcct gactaccatt ttatagacca ccgcattgag attatggagc atgacgagga ctacaaccat gtcaagctgc gcgagtgtgc tgtagctcgc tattctctgc tgcctgagaa gaacaagggt aagcctatcc ctaaccctct cctcggactc
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                                                                                               480
                                                                                               540
gattctacgc gtaccggtta g
                                                                                               561
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<211> 186
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Ala Asp Ile Pro Asp Tyr Ile Lys Leu Ser Phe Pro Glu Gly Phe Thr
Trp Glu Arg Ile Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr 35 40 45
Ser Asp Ile Ser Val Lys Gly Asp Ser Phe Tyr Tyr Lys Ile His Phe 50 60
Thr Gly Glu Phe Pro Pro Asn Gly Pro Val Met Gln Arg Arg Ile Arg 65 70 75 80
Gly Trp Glu Pro Ser Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu
85 90 95
Glu Gly His Asp Asp Met Thr Leu Arg Val Glu Gly Gly Gly His Tyr
100 105 110
Thr Cys Val Phe Lys Thr Ile Tyr Arg Ser Lys Lys Lys Val Glu Asn
115 120 125
Met Pro Asp Tyr His Phe Ile Asp His Arg Ile Glu Ile Met Glu His
                                135
Asp Glu Asp Tyr Asn His Val Lys Leu Arg Glu Cys Ala Val Ala Arg
                           150
                                                      155
Tyr Ser Leu Leu Pro Glu Lys Asn Lys Gly Lys Pro Ile Pro Asn Pro
165 170 175
Leu Leu Gly Leu Asp Ser Thr Arg
                180
<210> 113
<211> 720
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
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tctcttgaag tggtgaatgg cgcgcctctg ccgtttggtt ggcatatatt gtcaccagca
                                                                                                60
                                                                                               120
                                                                                               180
                                                    Page 55
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240
tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag
cagacctttc ctgaaggcta tcactgggag cgaataatgā cttttgagga cgggggcgta
                                                                                    300
tgttgcatca caagcgacat cagtatgaaa agtaacaact gtttcttcta tgacattaag
                                                                                    360
                                                                                    420
ticactggca tgaacittcc tcctaaiggt ccagtgatgc agaggaggat acgaggatgg
gagccatcca ctgaacgatt gtatcttcgc gacggtgtgc tgacgggaga tgtcaacatggctctgttgc ttaaagatgg ccgccatttg agagttgact ttaacacttc ttacataccc
                                                                                    480
                                                                                    540
āagaagaagg tcgagāatāt gcctgactac cattttātag accaccgcat tgagattctg
                                                                                    600
ggcaacccag aagacaagcc ggtcaagctg tacgagattg ctacagctcg ccatcatggg
ctgaagggta agcctatccc taaccctctc ctcggactcg attctacgcg taccggttag
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<211> 239
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<223> Synthetically generated
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Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala
Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Ala Phe Met Tyr Gly 50 55 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
GÎN Thr Phe Pro Glu GÎy Tyr His Trp Glu Arg Ile Met Thr Phe Glu
85 90 95
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Met Lys Ser Asn 100 105 110
Asn Cys Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe Pro Pro 115 120 125
Asn Gly Pro Val Met Gln Arg Arg Ile Arg Gly Trp Glu Pro Ser Thr
130 140
Glu Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly Asp Val Asn Met
145 150 155 160
Ala Leu Leu Lys Asp Gly Arg His Leu Arg Val Asp Phe Asn Thr
165 170 175
Ser Tyr Ile Pro Lys Lys Lys Val Glu Asn Met Pro Asp Tyr His Phe
180 185 190
Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val
195 200 205
Lys Leu Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly Lys 210 215 220
Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly 235
<210> 115
<211> 723
<212> DNA
<213> Artificial Sequence
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                                                                                     60
                                                                                    120
tctcttgaag tggtgaatgg cgcgcctctg acgttttctt tcgatgtatt gacaccagca
                                                                                    180
tttcagtatg gaaaccgtac attcaccaaa tacccaaaag agataccaga ctatttcaag
                                                                                    240
cagacettte etgaaggeta teaetgggag egaataatga ettttgagga egggggegta
                                                                                    300
                                              Page 56
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360
tgttgcatca caagcgacat cagtgtgaaa ggtgactctt tcttctatga cattaagttc
                                                                                 420
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ccatccactg aacgattgta tcttcgcgac ggtgtgctga cgggagatgt caacatggct ctgttgctta aagatggcgg ccattacaca tgtgtctta aaactattta cagatccaag aagaaggtcg agaatatgcc tgactaccat tttatagacc accgcattga gattatggag
                                                                                 480
                                                                                 540
                                                                                 600
                                                                                 660
catgacgagg actacaacca tgtcaagctg cgcgagattg ctacagctcg ccatcatggg
                                                                                 720
ctgaagggta agcctatccc taaccctctc ctcggactcg attctacgcg taccggtagc
                                                                                 723
tcq
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<223> Synthetically generated
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20 25 30 30
Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala
35 40 45
Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala Phe Gln Tyr Gly 50 60
Asn Arg Thr Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe 65 70 75
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
85 90 95
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val
                                                           Lys Gly Asp
                                     105
                                                            110
    Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe Pro Pro Asn
                                120
                                                        125
         115
Gly Pro Val Met Gln Arg Arg Ile Arg Gly Trp Glu Pro Ser Thr Glu
130 135 140
     130
Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly Asp Val Asn Met Ala
145 150 155 160
                       150
Leu Leu Leu Lys Asp Gly Gly His Tyr Thr Cys Val Phe Lys Thr Ile
165 170 175
Tyr Arg Ser Lys Lys Lys Val Glu Asn Met Pro Asp Tyr His Phe Ile
                                     185
Asp His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn His Val
    Leu Arg Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly Lys 210 215 220 ____
Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
225
                       230
Ser
<210> 117
<211> 717
<212> DNA
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                                                                                 120
tctcttgaag tggtgaatgg cgcgcctctg acgttttctt tcgatgtatt gacaccagca
                                                                                 180
                                                                                 240
tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag
                                             Page 57
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cagacctttc ctgaaggcta tcactgggag cgaataatga cttttgagga cgggggcgta
tgttgcatca caagcgacat cagtgtgaaa ggtgactctt tctactataa gattcacttc
                                                                                      300
                                                                                      360
actggcgagt ttcctcctca tggtccagtg atgcagagaa agacagtaaa atgggagcca
                                                                                      420
                                                                                      480
tccactgaac gattgtatct tcgcgacggt gtgctgacgg gacatgacga catgactctg
cgggttgaag gtggcggcca ttacacatgt gtctttaaaa ctatttacag atccaagaag aaggtcgaga atatgcctga ctaccatttt atagaccacc gcattgagat tatggagcat
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                                                                                      600
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<210> 118
<211> 238
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<220>
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Thr Val Asn Gly Asp Lys Phe Thr Ile Lys Gly Glu Gly Gly Tyr
Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala 35 40 45
Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala Phe Met Tyr Gly 50 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gin Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu 85 90 95
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp 100 105
Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His Gly
115 120 125
Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu Arg
130 135 140
Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly His Asp Asp Met Thr Leu 145 150 155 160
Arg Val Glu Gly Gly His Tyr Thr Cys Val Phe Lys Thr Ile Tyr
165 170 175
Arg Ser Lys Lys Val Glu Asn Met Pro Asp Tyr His Phe Ile Asp
His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn His Val Lys
195 200 205
Leu Arg Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly Lys Pro
Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly 225 235
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tetettgaag tggtgaatgg cgcgcctctg ccgttttett tcgatatatt gacaccagca
                                                                                      120
                                                                                      180
tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag
                                                                                      240
cagacette etgaaggeta teactgggag cgaataatga ettttgagga egggggegta
                                                                                      300
tgitgcatca caagcgacat cagtaigaaa agtaacaact gittciicta igacattaag
                                                                                      360
                                               Page 58
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ttcactggca tgaactttcc tcctaatggt ccagtgatgc agaggaggat acgaggatgg
                                                                                  420
gagccatcca ctgaaaacat ttatcctcgc gacgaatttc tggagggaga tgtcaacatg
                                                                                  480
gctctgttgc ttaaagatgg cggctattac agagctgaat ttagaagttc ttacaaaggc
aagaagaagg tcgagaatat gcctgactac cattttatag accaccgcat tgagattatg
gagcatgacg aggactacaa ccatgtcaag ctgcgcgaga ttgctacagc tcgccatcat
                                                                                  540
                                                                                  600
                                                                                  660
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                                                                                  720
<210> 120
<211> 240
<212> PRT
<213> Artificial Sequence
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<223> Synthetically generated
<400> 120
Met Lys Gly Val Lys Glu Val Met Lys Ile Ser Leu Glu Met Asp Cys

1 10 15
Thr Val Asn Gly Asp Lys Phe Thr Ile Lys Gly Glu Gly Gly Tyr
20 25 30
Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala
35 40 45
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
90 95
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Met Lys Ser Asn 100 105 110
Asn Cys Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe Pro Pro
115 120 125
Asn Gly Pro Val Met Gln Arg Arg Ile Arg Gly Trp Glu Pro Ser Thr
130 135 140
Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val Asn Met
145 150 155 160
Ala Leu Leu Lys Asp Gly Gly Tyr Tyr Arg Ala Glu Phe Arg Ser
165 170 175
Ser Tyr Lys Gly Lys Lys Lys Val Glu Asn Met Pro Asp Tyr His Phe
180 185 190
Ile Asp His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn His 195 200 205
Val Lys Leu Arg Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly 210 220
Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly 225 230 235 240
<210> 121
<211> 639
<212> DNA
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<223> Synthetically generated
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                                                                                  120
gggcctctgc cgtttggttg gcatatattg tcaccagcat ttatgtatgg aaaccgtgta
ttcaccaaat acccagccga tataccagac tatatcaagc tgtcctttcc tgagggcttt
                                                                                  180
                                                                                  240
acctgggagc gaagcattcc ttttcaagac caggcctcat gtaccgtcac aagcgacatc
                                                                                  300
agtgtgaaag gtgactcttt cttctatgac attaagttca ctggcatgaa ctttcctcct
                                                                                  360
aatggtccag tgatgcagag gaggatacga ggatgggagc catccactga acgattgtat
                                                                                  420
                                             Page 59
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cttcgcgacg gtgtgctgac gggacatgac gacatgactc tgcgggttga aggtggcggc
                                                                                  480
cattacacat gtgtctttaa aactatttac agatccaagc actcgatcaa catgccggat
ttccatttta tagaccaccg cattgatatt cggaagttcg acgaaaatta catcaacgtc
                                                                                  540
                                                                                  600
                                                                                  639
agcaggacga gattgctaca gctcgccatc atgggctga
<210> 122
<211> 212
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 122
Met Met Thr Asp Leu His Leu Asp Cys Thr Val Asn Gly Asp Lys Phe
Thr Ile Lys Gly Glu Gly Gly Gly Tyr Pro Tyr Glu Gly Thr Asn Phe 20 25 30
        Leu Val Val Thr Lys Gly Gly Pro Leu Pro Phe Gly Trp His 35 40 45
Ile Leu Ser Pro Ala Phe Met Tyr Gly Asn Arg Val Phe Thr Lys Tyr
                            55
Pro Ala Asp Ile Pro Asp Tyr Ile Lys Leu Ser Phe Pro Glu Gly Phe 65 70 75 80
Thr Trp Glu Arg Ser Ile Pro Phe Gln Asp Gln Ala Ser Cys Thr Val
85 90 95
Thr Ser Asp Ile Ser Val Lys Gly Asp Ser Phe Phe Tyr Asp Ile Lys
100 105 110
Phe Thr Gly Met Asn Phe Pro Pro Asn Gly Pro Val Met Gln Arg Arg
Ile Arg Gly Trp Glu Pro Ser Thr Glu Arg Leu Tyr Leu Arg Asp Gly
                            135
Val Leu Thr Gly His Asp Asp Met Thr Leu Arg Val Glu Gly Gly 145 150 155
    Tyr Thr Cys Val Phe Lys Thr Ile Tyr Arg Ser Lys His Ser Ile
165 170 175
Asn Met Pro Asp Phe His Phe Ile Asp His Arg Ile Asp Ile Arg Lys
              180
                                     185
Phe Asp Glu Asn Tyr Ile Asn Val Ser Arg Thr Arg Leu Leu Gln Leu 195 200 205
Ala Ile Met Gly
    210
<210> 123
<211> 714
<212> DNA
<213> Artificial Sequence
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                                                                                  120
tctcttgaag tggtgaatgg cgcgcctctg acgttttctt tcgatgtatt gacaccagca
tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag
                                                                                  180
                                                                                  240
cagacctttc ctgaaggcta tcactgggag cgaaaaatga cttatgagga cgggggcata
                                                                                  300
agtaacgtcc gaagcgacat cagtatgaaa agtaacaact gtttctacta taagattcac
                                                                                  360
ttcactggcg agtitcctcc tcatggicca gigatgcaga gaaagacagt aaaaigggag
                                                                                  420
ccatccactg aaaacattta tcctcgcgac gaatttctgg agggagatgt caacatggct
ctgttgctta aagatggcgg ccattacaca tgtgtcttta aaactattta cagatccaag
                                                                                  480
                                                                                  540
cactogatca acatgoogga tttccatttt atagaccacc gcattgagat totgggcaac
                                                                                  600
ccagaagaca agccggtcaa gctgtacgag attgctacag ctcgccatca tgggctgaag
                                                                                  660
                                                                                  714
ggtaagccta tccctaaccc tctcctcgga ctcgattcta cgcgtaccgg ttag
                                             Page 60
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<210> 124
<211> 237
<212> PRT
<213> Artificial Sequence
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<400> 124
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Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala
Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala Phe Met Tyr Gly 50 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Lys Met Thr
85 90
Asp Gly Gly Ile Ser Asn Val Arg Ser Asp Ile Ser Met Lys Ser Asn
             100
                                    105
Asn Cys Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His
                                120
                                                       125
Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu
130 135 140
Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val Asn Met Ala
145 150 156
Leu Leu Leu Lys Asp Gly Gly His Tyr Thr Cys Val Phe Lys Thr Ile
165 170 175
Tyr Arg Ser Lys His Ser Ile Asn Met Pro Asp Phe His Phe Ile Asp
                                    185
His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val Lys Leu
                                200
Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly Lys Pro Ile
210 215 220
Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg 225 230 235
<210> 125
<211> 714
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
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                                                                                 60
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tctcttgaag tggtgaatgg cgcgcctctg ccgtttggtt ggcatatatt gtcaccagca
                                                                                120
                                                                                180
tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag
                                                                                240
cagacettte etgaaggeta teaetgggag egaataatga ettttgagga egggggegta
                                                                                300
tgttgcatca caagcgacat cagtgtgaaa ggtgactctt tcttctatga cattaagttcactggcatga actttcctcc tcatggtcca gtgatgcaga gaaagacagt aaaatgggag
                                                                                360
                                                                                420
ccatccactg aaaacattta tcctcgcgac gaatttctgg agggagatgt caacatggct
                                                                                480
ctgttgctta aagatggcgg ccattacaca tgtgtcttta aaactattta cagatccaag
                                                                                540
cactcgatca acatgccgga tttccatttt atagaccacc gcattgagat tctgggcaac
                                                                                600
ccagaagaca agccggtcaa gctgtacgag attgctacag ctcgccatca tgggctgaag
                                                                                660
ggtaagccta tccctaaccc tctcctcgga ctcgattcta cgcgtaccgg ttag
                                                                                714
<210> 126
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<211> 237
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<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 126
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1 10 15
Thr Val Asn Gly Asp Lys Phe Thr Ile Lys Gly Glu Gly Gly Gly Tyr
20 25 30
Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala
Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Ala Phe Met Tyr Gly 50 55 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 75 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
85 90 95
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp 100 105 110
Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe Pro Pro His
                                  120
Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu
130 135 140
Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val Asn Met Ala
145 150 160
Leu Leu Leu Lys Asp Gly Gly His Tyr Thr Cys Val Phe Lys Thr Ile
165 170 175
Tyr Arg Ser Lys His Ser Ile Asn Met Pro Asp Phe His Phe Ile Asp
His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val Lys Leu
          195
                                  200
                                                            205
Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly Lys Pro Ile
210 215 220
Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly 225 230 235
<210> 127
<211> 741
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
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                                                                                       120
                                                                                       180
                                                                                       240
gačtatttca agcagacčtt tččtgaaggc tatcactggg agcgaataat gačťtttgag
                                                                                       300
gacgggggcg tatgttgcat cacaagcgac atcagtatga aaagtaacaa ctgtttcttc
                                                                                       360
ťatgačaťta agtťcačtgg catgaácťtt cctcčtcaťg gtcčagtgat gcágagaaag acagtaaaat gggagccatc cactgaagta atgtatgttg acgacaagag tgacggtgtg
                                                                                       420
                                                                                       480
ctgaagggag atgtcaacat ggctctgttg cttaaagatg gccgccattt gagagttgac
                                                                                       540
tttaacactt cttacatacc caagcactcg atcaacatgc cggatttcca ttttatagac
                                                                                       600
caccgcattg agattatgga gcatgacgag gactacaacc atgtcaagct gcgcgagatt gctacagctc gccatcatgg gctgaagggt aagcctatcc ctaaccctct cctcggactc
                                                                                       660
                                                                                       720
gattctacgc gtaccggtta g
                                                                                       741
<210> 128
<211> 246
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<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
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His Leu Glu Gly Thr Phe Asn Gly His Lys Phe Thr Ile Lys Gly Glu 20 25 30
Gly Gly Gly Tyr Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val
Val Asn Gly Ala Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala 50 60
Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Lys Glu Ile Pro 65 70 75 80
Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile
Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser
100 105 110
Met Lys Ser Asn Asn Cys Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met
                                  120
Asn Phe Pro Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp
                                                       140
                              135
Glu Pro Ser Thr Glu Val Met Tyr Val Asp Asp Lys Ser Asp Gly Val
145 150 155
Leu Lys Gly Asp Val Asn Met Ala Leu Leu Leu Lys Asp Gly Arg His 165 170 175
Leu Arg Val Asp Phe Asn Thr Ser Tyr Ile Pro Lys His Ser Ile Asn 185 190
Met Pro Asp Phe His Phe Ile Asp His Arg Ile Glu Ile Met Glu His 195 200 205
                                   200
          195
Asp Glu Asp Tyr Asn His Val Lys Leu Arg Glu Ile Ala Thr Ala Arg
                              215
                                                       220
His His Gly Leu Lys Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu
225 230 235 240
Asp Ser Thr Arg Thr Gly
 <210> 129
 <211> 723
 <212> DNA
 <213> Artificial Sequence
 <223> Synthetically generated
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                                                                                       120
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 catcttacag agaaggaagg caagcctctg ccgtttggtt ggcatatatt gtcaccacaa ttacagtatg gaaacaagtc attcgtcagc tacccaaaag agataccaga ctatttcaag cagacctttc ctgaaggcta tcactgggag cgaaaaatga cttatgagga cgggggcata
                                                                                       180
                                                                                        240
                                                                                        300
 agtaacgtcc gaagccacat caggatgaaa gaggaagagg agcggcattt ctactataag
                                                                                        360
 attcacttca ctggcgagtt tcctcctcat ggtccagtga tgcagagaaa gacagtaaaa
                                                                                        420
 tgggagccat ccactgaacg attgtatctt cgcgacggtg tgctgacggg acatgacgac atgactctgc gggttgaagg tggccgcat ttgagagttg actttaacac ttcttacata cccaagaaga aggtcgagaa tatgcctgac taccattta tagaccaccg cattgagatt
                                                                                        480
                                                                                        540
                                                                                        600
 ctgggcaacc cagaagacaa gccggtcaag ctgtacgaga ttgctacagc tcgccatcat
                                                                                        660
 gggctgaagg gtaagcctat ccctaaccct ctcctcggac tcgattctac gcgtaccggt
                                                                                        720
                                                                                        723
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<211> 240
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 130
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                                             10
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Pro Tyr Glu Gly Thr Gln Thr Leu His Leu Thr Glu Lys Glu Gly Lys 35 40 45
Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Gln Leu Gln Tyr Gly 50 _ _ _ 60
Asn Lys Ser Phe Val Ser Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
GIn Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Lys Met Thr Tyr Glu
85 90 95
                    85
Asp Gly Gly Ile Ser Asn Val Arg Ser His Ile Arg Met Lys Glu Glu 100 105 110
Glu Glu Arg His Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro
115 120 125
Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser
                                                       140
                              135
     130
Thr Glu Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly His Asp Asp
                                                  155
                         150
Met Thr Leu Arg Val Glu Gly Gly Arg His Leu Arg Val Asp Phe Asn
                                             170
Thr Ser Tyr Ile Pro Lys Lys Lys Val Glu Asn Met Pro Asp Tyr His
                                                                 190
                                        185
               180
Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro
195 200 205
     Lys Leu Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly
                              215
                                                       220
Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly 225 235 240
                         230
<210> 131
<211> 717
<212> DNA
<213> Artificial Sequence
<223> Synthetically generated
<221> unsure
<222> 6
<223> N is A, G, C or T
<221> unsure
<222> 32
<223> N is A, G, C or T
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                                                                                         60
                                                                                        120
                                                                                        180
                                                                                        240
                                                                                        300
cagacctttc ctgaaggcta tcactgggag cgaataatga cttttgagga cgggggcgta
tgttgcatca caagcgacat cagtgtgaaa ggtgactctt tctactataa gattcacttc
                                                                                        360
actggcgagt ttcctcctca tggtccagtg atgcagagaa agacagtaaa atgggagcca
tccactgaaa acatttatcc tcgcgacgaa tttctggagg gagatgtcaa catggctctg
                                                                                        420
                                                                                        480
                                                Page 64
```

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540
ttgcttaaag atggcggcta ttacagagct gaatttagaa gttcttacaa aggcaagaag
aaggtcgaga atatgcctga ctaccatttt atagaccacc gcattgagat tatggagcat
                                                                              600
gacgaggact acaaccatgt caagctgcgc gagattgcta cagctcgcca tcatgggctg
                                                                              660
                                                                              717
aagggtaagc ctatccctaa ccctctcctc ggactcgatt ctacgcgtac cggttag
<210> 132
<211> 238
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
<221> UNSURE
<222> 2
<223> Xaa is Lys or Asp
<221> UNSURE
<222> 11
<223> Xaa is Ile, Asp, Ser, or Thr
<400> 132
Met Xaa Gly Val Lys Glu Val Met Lys Ile Xaa Leu Glu Met Glu Gly
                                       10
Ala Val Asn Gly His His Phe Thr Ile Lys Gly Glu Gly Gly Tyr
Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala
35 40 45
Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Ala Phe Met Tyr Gly 50 55 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
                 85
                                       90
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp
                                   105
Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His Gly 115 120 125
Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu Asn
    130
                          135
                                                140
Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val Asn Met Ala Leu
145 150 155 160
                                                                  160
Leu Leu Lys Asp Gly Gly Tyr Tyr Arg Ala Glu Phe Arg Ser Ser Tyr
165 170 175
Lys Gly Lys Lys Val Glu Asn Met Pro Asp Tyr His Phe Ile Asp
180 185 190
His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn His Val Lys
                                                     205
                              200
Leu Arg Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly Lys Pro
                          215
Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
                      230
<210> 133
<211> 732
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
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                                                                              60
                                                                             120
                                          Page 65
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ggatgggagc catccactga agtaatgtat gttgacgaca agagtgacgg tgtgctgaag
ggacatgacg acatgactct gcgggttgaa ggtggccgcc atttgagagt tgactttaac
acttettaca tacceaagea etegateaac atgeeggatt tecattttat agaceaeege attgagatte tgggeaacee agaagacaag eeggteaage tgtaegagat tgetaeaget
cgccatcatg ggctgaaggg taagcctatc cctaaccctc tcctcggact cgattctacg
cgtaccggtt ag
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<211> 243
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
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His Leu Glu Gly Thr Phe Asn Gly His Lys Phe Thr Ile Lys Gly Glu
Gly Gly Tyr Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val
35 40
Val Asn Gly Ala Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala 50 55 60
Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Lys Glu Ile Pro 65 70 75 80
Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Île
Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser
100 105 110
Val Lys Gly Asp Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe
115 120 125
Pro Pro Asn Gly Pro Val Met Gln Arg Arg Ile Arg Gly Trp Glu Pro
130 135 140
Ser Thr Glu Val Met Tyr Val Asp Asp Lys Ser Asp Gly Val Leu Lys
150 155 160
Gly His Asp Asp Met Thr Leu Arg Val Glu Gly Gly Arg His Leu Arg
165 170 175
Val Asp Phe Asn Thr Ser Tyr Ile Pro Lys His Ser Ile Asn Met Pro
180 185 190
Asp Phe His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu 195 200 205
Asp Lys Pro Val Lys Leu Tyr Glu Ile Ala Thr Ala Arg His His Gly 210 220
Leu Lys Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser
225
                       230
Arg Thr Gly
<210> 135
<211> 717
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 135
atgaaggggg tgaaggaagt aatgaagatc agtctggaga tggagggcgc tgttaacggc
                                            Page 66
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gtacagttta tgtctcttga agtggtgaat ggcgcgcctc tgccgttttc tttcgatata

ttgacaccag catttcagta tggaaaccgt acattcacca aatacccaaa agagatacca

gactatttca agcagacctt tcctgaaggc tatcactggg agcgaataat gacttttgag

gacgggggcg tätgťtgcat cacaagcgac atcagtgťga aaggtgactc ťttctacťať aagattcact tcactggcga gtttcctcct aatggtccag tgatgcagag gaggatacga

180

240

300

360 420

480

540

600 660

720

732

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caccactttg agatcgaagg ggagggaaac ggaaaacctt acgcaggagt acagtttatg
                                                                                                 120
 tctcttgaag tggtgaatgg cgcgcctctg ccgttttctt tcgatatatt gacaccagca tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag cagacctttc ctgaaggcta tcactgggag cgaataatga cttttgagga cggggggta tgttgcatca caagcgacat cagtgtgaaa ggtgacttt tctctatga cattaagttc
                                                                                                 180
                                                                                                 240
                                                                                                 300
                                                                                                 360
 actggcatga actitcctcc tcatggicca gigatgcaga gaaagacagt aaaatgggag
                                                                                                 420
 ccatccactg aaaacattta tcctcgcgac gaatttctgg agggagatgt caacatggct ctgttgctta aagatggcgg ccattacaca tgtgtcttta aaactattta cagatccaag cactcgatca acatgccgga tttccatttt atagaccacc gcattgagat tatggagcat gacgaggact acaaccatgt caagctgcgc gagattgcta cagctcgcca tcatgggctg
                                                                                                 480
                                                                                                 540
                                                                                                 600
                                                                                                 660
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                                                                                                 717
 <210> 136
 <211> 238
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetically generated
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Ala Val Asn Gly His His Phe Glu Ile Glu Gly Glu Gly Asn Gly Lys
Pro Tyr Ala Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala 35 40 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 ____ 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 _ 70 _ 75 _ 80
Gin Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
85 90 95
                                                 90
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp 100 105 110
Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe Pro Pro His
Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu
130 140
Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val Asn Met Ala
145 150 155 160
Leu Leu Lys Asp Gly Gly His Tyr Thr Cys Val Phe Lys Thr Ile
165 170 175
Tyr Arg Ser Lys His Ser Ile Asn Met Pro Asp Phe His Phe Ile Asp 180 185 190
His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn His Val Lys
Leu Arg Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly Lys Gln 210 220
Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Gly Thr Gly
                           230
<210> 137
<211> 738
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
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                                                                                                 60
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gtacagttta tgtctcttga agtggtgaat ggcgcgcctc tgacgttttc tttcgatgta
                                                                                                120
                                                                                                180
                                                    Page 67
```

```
ttgacaccag catttatgta tggaaaccgt gtattcacca aatacccaaa agagatacca
                                                                                     240
 gactatttca agcagacctt tcctgaaggc tatcactggg agcgaataat gacttttgag
                                                                                     300
gacgggggcg tatgttgcat cacaagcgac atcagtgtga aaggtgactc tttcttctat gacattaagt tcactggcat gaactttcct cctcatggtc cagtgatgca gagaaagaca gtaaaatggg agccatccac tgaacgattg tatcttcgcg acggtgtgct gacgggacat
                                                                                     360
                                                                                     420
                                                                                     480
 gacgacatga ctctgcgggt tgaaggtggc cgccatttga gagttgactt taacacttct
                                                                                     540
tacătaccca agcactcgăt căacătgccg gătttccatt ttatagacca ccgcattgag attctgggca acccagaaga caagccggtc aagctgtacg agtgtgctgt agctcgctat
                                                                                     600
                                                                                     660
 tctctgctgc ctgagaagaa caagggtaag cctatcccta accctctcct cggactcgat
                                                                                     720
tctacgcgta ccggttag
                                                                                     738
<210> 138
<211> 245
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 138
Met Ser His Ser Lys Ser Val Ile Lys Asp Glu Met Phe Ile Lys Ile
1 10 15
    Leu Glu Gly Thr Phe Asn Gly His Lys Phe Thr Ile Lys Gly Glu
Gly Gly Gly Tyr Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val
35 40 45
    Asn Gly Ala Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala 50 _ _ _ 60 _ _ _ _
Phe Met Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro 65 70 75 80
Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile
85 90 _ 95
Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser
                                      105
                                                               110
Val Lys Gly Asp Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn 115 120 125
Phe Pro Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu
     130
                             135
Pro Ser Thr Glu Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly His
145 150 155 160
Asp Asp Met Thr Leu Arg Val Glu Gly Gly Arg His Leu Arg Val Asp
                   165
                                           170
                                                                   175
Phe Asn Thr Ser Tyr Ile Pro Lys His Ser Ile Asn Met Pro Asp Phe
              180
                                      185
                                                               190
His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys
                                 200
                                                          205
Pro Val Lys Leu Tyr Glu Cys Ala Val Ala Arg Tyr Ser Leu Leu Pro
     210
                             215
                       Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp
230 235 240
<210> 139
<211> 729
<212> DNA
<213> Artificial Sequence
<223> Synthetically generated
<400> 139
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acttttaacg gccacaaatt tacgatcaaa ggggaaggag gaggataccc ttacgaagga
                                                                                    120
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gtacagttta tgtctcttga agtggtgaat ggcgcgcctc tgacgttttc tttcgatgta
                                                                                    180
 ttgacaccag catttatgta tggaaaccgt gtattcacca aatacccaaa agggatacca gactattca agcagacctt tcctgaaggc tatcactggg agcgaataat gacttttgag
                                                                                     240
                                                                                    300
 gacgggggcg tatgttgcat cacaagcgac atcagtgtga aaggtgactc tttcttctat
                                                                                     360
 gacāttāāgt tcactggcat gaactttēct cctaātggtc cagtgātgca gaggaggata
                                                                                    420
 ctaggatggg agccatccac tgaacgattg tatcttcgcg acggtgtgct gacgggacat
                                                                                    480
gacgacatga ctctgcgggt tgaaggtggc ggccattaca catgtgtctt taaaactatt tacagatcca agaagaaggt cgagaatatg cctgactacc attttataga ccaccgcatt gagattctgg gcaacccaga agacaagccg gtcaagctgt acgagattgc tacagctcgc
                                                                                    540
                                                                                    600
                                                                                    660
 čatcatgggč tgaagggtāa gčctatčcct āaccctctčc tcggāctcga ttctācgcgt
                                                                                    720
 accggttag
                                                                                    729
 <210> 140
 <211> 242
 <212> PRT
 <213> Artificial Sequence
 <220>
<223> Synthetically generated
<400> 140
Met Ser His Ser Lys Ser Val Ile Lys Asp Glu Met Phe Ile Lys Ile
10 15
His Leu Glu Gly Thr Phe Asn Gly His Lys Phe Thr Ile Lys Gly Glu 20 25 30
Gly Gly Gly Tyr Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val
45
40
     Asn Gly Ala Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala 50 55 60
Phe Met Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Lys Gly Ile Pro 65 70 75 80
Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile
85 90 ____ 95
Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser
Val Lys Gly Asp Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn 115 120 125
Phe Pro Pro Asn Gly Pro Val Met Gln Arg Arg Ile Leu Gly Trp Glu
     130
                            135
    Ser Thr Glu Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly His
150 155 160
Asp Asp Met Thr Leu Arg Val Glu Gly Gly Gly His Tyr Thr Cys Val
165 170 175
Phe Lys Thr Ile Tyr Arg Ser Lys Lys Lys Val Glu Asn Met Pro Asp
Tyr His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp
                                 200
Lys Pro Val Lys Leu Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu
                            215
Lys Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr 235
Thr Gly
<210> 141
<211> 726
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 141
atgaaggggg tgaaggaagt aatgaagatc agtctggaga tggactgcac tgttaacggc
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gacaaattta cgatc<u>aaagg</u> ggaaggagga ggataccctt acgaaggagt acagtttatg
tctcttgaag tggtgaatgg cgcgcctctg ccgttttctt tcgatatatt gacaccacaa
ttacagtatg gaaacaagtc attcgtcagc tacccaaaag agataccaga ctatttcaag cagacctttc ctgaaggcta tcactgggag cgaataatga cttttgagga cggggggta tgttgcatca caagccacat caggatgaaa gaggaagagg agcggcattt cttctatgac
attaagttca ctggcatgaa ctttcctcct catggtccag tgatgcagag aaagacagta
aaatgggagc catccactga aaacatttat cctcgcgacg aatttctgga gggacatgac
gacatgactc tgcgggttga aggtggccgc catttgagag ttgactttaa cacttcttac atacccaagc actcgatcaa catgccggat ttccatttta tagaccaccg cattgagatt atggagcatg acgaggacta caaccatgtc aagctgcgcg agattgctac agctcgccat
catgggctga agggtaagcc tatccctaac cctctcctcg gactcgattc tacgcgtacc
ggttag
<210> 142
<211> 241
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 142
Met Lys Gly Val Lys Glu Val Met Lys Ile Ser Leu Glu Met Asp Cys
Thr Val Asn Gly Asp Lys Phe Thr Ile Lys Gly Glu Gly Gly Gly Tyr 20 25 30
Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala 35 40 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Gln Leu Gln Tyr Gly 50 55
Asn Lys Ser Phe Val Ser Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
                    85
                                             90
Asp Gly Gly Val Cys Cys Ile Thr Ser His Ile Arg Met Lys Glu Glu 100 105 110
Glu Glu Arg His Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe
115 120 125
Pro Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro
                              135
Ser Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly His Asp
145 150 155
Asp Met Thr Leu Arg Val Glu Gly Gly Arg His Leu Arg Val Asp Phe
165 170 175
Asn Thr Ser Tyr Ile Pro Lys His Ser Ile Asn Met Pro Asp Phe His
180 185 190
Phe Ile Asp His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn
                                   200
                                                             205
His Val Lys Leu Arg Glu Ile Ala Thr Ala Arg His His Gly Leu Lys
                              215
                                                       220
Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr 225 230 235 240
                                                  235
ĞĪy
<210> 143
<211> 732
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 143
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120

180

240 300 360

420

480

540 600 660

720

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 gacaaatttg agatcgaagg ggagggaaac ggaaaacctt acgcaggagt acagtttatg
 tctcttgaag tggtgaatgg cgcgcctctg ccgttttctt tcgatatatt gacaccacaa ttacagtatg gaaacaagtc attcgtcagc tacccagccg atataccaga ctatatcaag ctgtcctttc ctgaggggctt tacctgggag cgaagcattc ctttcaaga ccaggcctca
 tgtaccgtca caagccacat caggatgaaa gaggaagagg agcggcattt ctactataag
 attcacttca ctggcgagtt tcctcctcat ggtccagtga tgcagagaaa gacagtaaaa
 tgggagccat ccactgaacg attgtatctt cgcgacggtg tgctgacggg agatgtcaac
atggctctgt tgcttaaaga tggccgccat ttgagagttg actttaacac ttcttacata cccaagcact cgatcaacat gccggatttc cattttatag accaccgcat tgagattctg ggcaacccag aagacaagcc ggtcaagctg tacgagtgtg ctgtagctcg ctattctctg ctgcctgaga agaacaaggg taagcctatc cctaaccctc tcctcggact cgattctacg
 cgtaccggtt ag
 <210> 144
 <211> 243
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetically generated
 <400> 144
Met Lys Gly Val Lys Glu Val Met Lys Ile Ser Leu Glu Met Asp Cys 10 10 15
Thr Val Asn Gly Asp Lys Phe Glu Ile Glu Gly Glu Gly Asn Gly Lys
Pro Tyr Ala Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Gln Leu Gln Tyr Gly 50 60
Asn Lys Ser Phe Val Ser Tyr Pro Ala Asp Ile Pro Asp Tyr Ile Lys 70 75 80
Leu Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Ser Ile Pro Phe Gln 85 90 95
Asp Gln Ala Ser Cys Thr Val Thr Ser His Ile Arg Met Lys Glu Glu
100 105 110
Glu Glu Arg His Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro
125
Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser
Thr Glu Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly Asp Val Asp
                         150
                                                  155
Met Ala Leu Leu Lys Asp Gly Arg His Leu Arg Val Asp Phe Asn
                                             170
Thr Ser Tyr Ile Pro Lys His Ser Ile Asn Met Pro Asp
                                        185
Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val
                                   200
Lys Leu Tyr Glu Cys Ala Val Ala Arg Tyr Ser Leu Pro Glu Lys
                             215
                                                      220
Asn Lys Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser
Arg Thr Gly
<210> 145
<211> 717
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
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60

120

180 240 300

360

420

480

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<400> 145
 atgaaggggg tgaaggaagt aatgaagatc agtctggaga tggactgcac tgttaacggc
                                                                                               60
gacaaatttg agatcgaagg ggagggaaac ggaaaacctt acgcaggagt acagtttatg tctcttgaag tggtgaatgg cgcgcctctg ccgttttctt tcgatatatt gacaccagca tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctattcaag cagacctttc ctgaaggcta tcactggaga cggagacattc ctgaaggcta
                                                                                              120
                                                                                             180
                                                                                             240
                                                                                              300
 tgttgcatca caagcgacat cagtgtgaaa ggtgactctt tcttctatga cattaagttc
                                                                                             360
 actggcatga actitectee teatggicea gigatgeaga gaaagacagt aaaatgggag
                                                                                             420
ccatccactg aacgattgta tcttcgcgac ggtgtgctga cgggagatgt caacatggct ctgttgctta aagatggcgg ccattacaca tgtgtcttta aaactattta cagatccaag aagaaggtcg agaatatgcc tgactaccat tttatagacc accgcattga gattctgggc aacccagaag acaagccggt caagctgtac gagattgcta cagctcgcca tcatgggctg
                                                                                             480
                                                                                             540
                                                                                             600
                                                                                             660
 aagggtaagc ctatccctaa ccctctcctc ggactcgatt ctacgcgtac cggttag
                                                                                             717
 <210> 146
 <211> 238
 <212> PRT
 <213> Artificial Sequence
<220>
 <223> Synthetically generated
<400> 146
Met Lys Gly Val Lys Glu Val Met Lys Ile Ser Leu Glu Met Asp Cys

10 15
Thr Val Asn Gly Asp Lys Phe Glu Ile Glu Gly Glu Gly Asn Gly Lys
Pro Tyr Ala Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala 35 40 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 _ 55 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
85 90 95
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp
100 105 110
Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe Pro Pro His
Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu
130 135 140
Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly Asp Val Asn Met Ala
Leu Leu Lys Asp Gly Gly His Tyr Thr Cys Val Phe Lys Thr Ile
165 170 175
Tyr Arg Ser Lys Lys Lys Val Glu Asn Met Pro Asp Tyr His Phe Ile
180 _____ 185 ____ 190
Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val Lys
Leu Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly Lys Pro
Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
<210> 147
<211> 513
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
ttgagatcga aggggaggga aacggaaaac cttacgcagg aacacagact ttacatctta
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cagagaagga aggcaagcct ctgccgtttg gttggcatat attgtcacca caattacagt
                                                                                               120
atggaaacaa gtcattcgtc agctacccag gcaatatacc agactttttc aagcagaccg
tttctggtgg cgggtatacc cactgaagta atgtatgttg acgacaagag tgacggtgtg
                                                                                               180
                                                                                               240
ctgaagggac atgacgacat gactctgcgg gttgaaggtg gccgccattt gagagttgactttaacactt cttacatacc caagcactcg atcaacatgc cggatttcca ttttatagac
                                                                                               300
                                                                                               360
                                                                                               420
caccgcattg atattcggaa gttcgacgaa aattacatca acgtcgagca ggacgagtgt
gctgtagctc gctattctct gctgcctgag aagaacaagg gtaagcctat ccctaaccct
ctcctcggac tcgattctac gcgtaccggt tag
                                                                                               480
                                                                                               513
<210> 148
<211> 170
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 148
Met Arg Ser Lys Gly Arg Glu Thr Glu Asn Leu Thr Gln Glu His Arg
                                                 10
Leu Tyr Ile Leu Gln Arg Arg Lys Ala Ser Leu Cys Arg Leu Val Gly
20 25 30
Ile Tyr Cys His His Asn Tyr Ser Met Glu Thr Ser His Ser Ser Ala
35 40 45
     Gln Ala Ile Tyr Gln Thr Phe Ser Ser Arg Pro Phe Leu Val Ala
50 _ _ 55 _ 60
Gly Ile Pro Thr Glu Val Met Tyr Val Asp Asp Lys Ser Asp Gly Val 80
Leu Lys Gly His Asp Asp Met Thr Leu Arg Val Glu Gly Gly Arg His
85 90 95
Leu Arg Val Asp Phe Asn Thr Ser Tyr Ile Pro Lys His Ser Ile Asn
100 105 110
     Pro Asp Phe His Phe Ile Asp His Arg Ile Asp Ile Arg Lys Phe 115 120 125
Asp Glu Asn Tyr Ile Asn Val Glu Gln Asp Glu Cys Ala Val Ala Arg
130 135 140
Tyr Ser Leu Leu Pro Glu Lys Asn Lys Gly Lys Pro Ile Pro Asn Pro 145 150 160
Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly
<210> 149
<211> 690
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 149
atgaaggggg tgaaggaagt aatgaagatc agtctggaga tggactgcac tgttaacggc
                                                                                                60
gacaaattta cgatcaaagg ggaaggagga ggataccctt acgaaggagt acagtttatg tctcttgaag tggtgaatgg cgcgcctctg ccgttttctt tcgatatatt gacaccagca tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag
                                                                                               120
                                                                                               180
                                                                                               240
cagacctttc ctgaaggcta ttactgggag cgaaaaatga cttatgagga cgggggcata
                                                                                               300
agtaacgtcc gaagcgacat cagtgtgaaa ggtgactctt tctactataa gattcacttc actggcgagt ttcctcctca tggtccagtg atgcagagaa agacagtaaa atgggagcca tccactgaaa acatttatcc tcgcgacgaa tttctggagg gagatgtcaa catggctctg
                                                                                               360
                                                                                               420
                                                                                               480
ttgcttāaag atggccgcca ttīgāgagīt gacttīāacā cītīctīacat acccaagaag
                                                                                               540
aaggtcgaga atatgcctga ctaccatttt atagaccacc gcattgagat tctgggcaac
                                                                                               600
ccagaagača agccggtcaa gctgtacgag attgctacag čtcgcčaťca tgggčťgaag
ggtaagccta tccctaaccc tctcctcgga
                                                                                               660
                                                                                               690
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<211> 230
<212> PRT
 <213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 150
Met Lys Gly Val Lys Glu Val Met Lys Ile Ser Leu Glu Met Asp Cys
1 10 15
                                            10
Thr Val Asn Gly Asp Lys Phe Thr Ile Lys Gly Glu Gly Gly Tyr
20 25 30
Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala
35 40 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 _ _ _ 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
65
Gln Thr Phe Pro Glu Gly Tyr Tyr Trp Glu Arg Lys Met Thr Tyr Glu
Asp Gly Gly Ile Ser Asn Val Arg Ser Asp Ile Ser Val Lys Gly Asp
100 105 110
Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His Gly
115 120 125
Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu Asn
130 135 140
Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val Asn Met Ala Leu
145 150 155 160
Leu Leu Lys Asp Gly Arg His Leu Arg Val Asp Phe Asn Thr Ser Tyr
165 170 175
Ile Pro Lys Lys Lys Val Glu Asn Met Pro Asp Tyr His Phe Ile Asp
              180
                                       185
                                                               190
His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val Lys Leu 195 _ 200 _ 205
Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly Lys Pro Ile
210 ____ 215 ___ 220
Pro Asn Pro Leu Leu Gly
<210> 151
<211> 393
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 151
atggaaaccg tacattcacc aaatacccag gcaatatacc agactttttc aagcagaccg
                                                                                      60
tttctggtgg cgggtatacc cactgaagta atgtatgttg acgacaagag tgacqqtqtq
                                                                                    120
ctgaagggag atgtcaacat ggctctgttg cttaaagatg gccgccattt gagagttgac
tttaacactt cttacatacc caagcactcg atcaacatgc cggatttcca ttttatagac
caccgcattg agattatgga gcatgacgag gactacaacc atgtcaagct gcgcgagtgt
                                                                                    180
                                                                                     240
                                                                                     300
gctgtagctc gctattctct gctgcctgag aagaacaagg gtaagcctat ccctaaccct
                                                                                     360
ctcctcggac tcgattctac gcgtaccggt tag
                                                                                    393
<210> 152
<211> 130
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
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<400> 152
Met Glu Thr Val His Ser Pro Asn Thr Gln Ala Ile Tyr Gln Thr Phe
Ser Ser Arg Pro Phe Leu Val Ala Gly Ile Pro Thr Glu Val Met Tyr
    Asp Asp Lys Ser Asp Gly Val Leu Lys Gly Asp Val Asn Met Ala
Leu Leu Lys Asp Gly Arg His Leu Arg Val Asp Phe Asn Thr Ser 50 55
Tyr Ile Pro Lys His Ser Ile Asn Met Pro Asp Phe His Phe Ile Asp 65 70 75 80
His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn His Val Lys
Leu Arg Glu Cys Ala Val Ala Arg Tyr Ser Leu Leu Pro Glu Lys Asn
                                      105
Lys Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg
Thr Gly
     130
<210> 153
<211> 750
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 153
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                                                                                   60
                                                                                  120
                                                                                  180
ttgacaccag catttatgta tggaaaccgt gtattcacca aatacccaaa agagatacca
                                                                                  240
gactatttca agcagacctt tcctgaaggc tatcactggg agcgaataat gacttttgag
                                                                                  300
gacgggggcg tatgttgcat cacaagccac atcaggatga aagaggaaga ggagcggcat
                                                                                  360
ttettetátő acattaágtt caetgőcatg aacttteete etéatógtée ágtgatójcag
                                                                                  420
agaaagacağ taaaatgöga gccatccact gaagtaatgt atgttgacga caağagtgac
                                                                                  480
gğtgtőctga agggagátgt caacatggct ctgītgctīa aagatggcgg ctaitacaga
                                                                                  540
gčtgaattīa gaagtīctīa caaaggcaag aagaaggtcg agaatatgcc tgactaccat
                                                                                  600
tttatagacc accgcattga gattatggag catgacgagg actacaacca tgtcaagctgcgcgagattg ctacagctcg ccatcatggg ctgaagggta agcctatccc taacctctc
                                                                                  660
                                                                                  720
ctcggactcg attctacgcg taccggttag
                                                                                  750
<210> 154
<211> 249
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 154
Met Ser His Ser Lys Ser Val Ile Lys Asp Glu Met Phe Ile Lys Ile
1 10 15
    Leu Glu Gly Thr Phe Asn Gly His Lys Phe Thr Ile Lys Gly Glu
20 25 30
Gly Gly Tyr Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val
35 40 45
   Asn Gly Ala Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala
Phe Met Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro 65 70 75 80
Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Île
85 90 95
```

```
Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser His Ile Arg
Met Lys Glu Glu Glu Glu Arg His Phe Phe Tyr Asp Ile Lys Phe Thr
115 120 125
Gly Met Asn Phe Pro Pro His Gly Pro Val Met Gln Arg Lys Thr Val
                             135
                                                    140
Lys Trp Glu Pro Ser Thr Glu Val Met Tyr Val Asp Asp Lys
                        150
                                               155
Gly Val Leu Lys Gly Asp Val Asn Met Ala Leu Leu Leu Lys
165 170
                                                                  Asp Gly
         Tyr Arg Ala Glu Phe Arg Ser Ser Tyr Lys Gly Lys Lys 180 185 190
Val Glu Asn Met Pro Asp Tyr His Phe Ile Asp His Arg Ile Glu Ile
195 200 205
Met Glu His Asp Glu Asp Tyr Asn His Val Lys Leu Arg Glu Ile Ala 210 220
Thr Ala Arg His His Gly Leu Lys Gly Lys
                                               Pro Ile Pro Asn Pro
235
225
                        230
Leu Gly Leu Asp Ser Thr Arg Thr Gly
<210> 155
<211> 720
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 155
atgaaggggg tgaaggaagt aatgaagatc agtctggaga tggactgcac tgttaacggc
                                                                                    60
gacaaattta cgatcaaagg ggaaggagga ggataccctt acgaaggagt acaqtttatq
                                                                                   120
tctcttgaag tggtgaatgg cgcgcctctg ccgttttctt tcgatatatt gacaccagca
                                                                                   180
tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag
                                                                                   240
cagacctttc ctgaaggcta tcactgggag cgaataatga cttttgagga cgggggcgta
                                                                                   300
tgttgcatca caagcgacat cagtatgaaa agtaacaact gtttcttcta tgacattaag tcactggca tgaactttcc tcctcatggt ccagtgatgc agagaaagac agtaaaatgg gagccatcca ctgaacgatt gtatcttcgc gacggtgtgc tgacgggaga tgtcaacatg
                                                                                   360
                                                                                   420
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gctctgttgc ttaaagatgg ccgccatttg agagttgact ttaacacttc ttacataccc
                                                                                   540
aagaagaagg tcgagaatat gcctgactac cattttatag accaccgcat tgagattctg
                                                                                   600
ggcaacccag aagacaagcc ggtcaagctg tacgagattg ctacagctcg ccatcatgggctgaagggta agcctatccc taaccctctc ctcggactcg attctacgcg taccggttag
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                                                                                   720
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<211> 239
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<220>
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Met Lys Gly Val Lys Glu Val Met Lys Ile Ser Leu Glu Met Asp Cys
10 15
Thr Val Asn Gly Asp Lys Phe Thr Ile Lys Gly Glu Gly Gly Tyr 20 25 30
Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala 35 40 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
                                             Page 76
```

```
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Met Lys Ser Asn 100 105 110
Asn Cys Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe Pro Pro
115 120 125
                                                           125
His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr
Glu Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly Asp Val Asn Met
145 150 155 160
Ala Leu Leu Lys Asp Gly Arg His Leu Arg Val Asp
                                                               Phe Asn Thr
                                             170
                                                                     175
Ser Tyr Ile Pro Lys Lys Lys Val Glu Asn Met Pro Asp Tyr His Phe
                                        185
Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val
    Leu Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly Lys 210 220
    Ile Pro Asn Pro Leu Leu Gly Leu Asp
                                                      Thr Arg Thr Gly
<210> 157
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<212> DNA
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<220>
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                                                                                      120
tctcttgaag tggtgaatgg cgcgcctctg ccgttttctt tcgatatatt gacaccagca
tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag
                                                                                      180
                                                                                      240
cagacctttc ctgaaggcta tcactgggag cgaaaaatgā cttatgagga cgggggcatā
                                                                                      300
agtaacgtcc gaagcgacat cagtgtgaaa ggtgactctt tcttctatga cattaagttc
                                                                                      360
actggcātga āctttcctcc taātggtcca gtgatgcaga ggaggatacg aggatgggag
                                                                                      420
ccatccactg aagtaatgta tgttgacgac aagagtgacg gtgtgctgaa gggagatgtc aacatggctc tgttgcttaa agatggccgc catttgagag ttgactttaa cacttcttac atacccaaga agaaggtcga gaatatgcct gactaccatt ttatagacca ccgcattgag attctgggca acccagaaga caagccggtc aagctgtacg agtgtgctgt agctcgctat
                                                                                      480
                                                                                      540
                                                                                      600
                                                                                      660
tctctgctgc ctgagaagaa caagggtaag cctatcccta accctctcct cggactcgat
                                                                                      720
tctacgcgta ccggttag
                                                                                      738
<210> 158
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Thr Val Asn Gly Asp Lys Phe Thr Ile Lys Gly Glu Gly Gly Gly Tyr
Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala
35 40 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 _ _ _ 60 _ _ .
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gin Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Lys Met Thr
                                            90
Asp Gly Gly Ile Ser Asn Val Arg Ser Asp Ile Ser Val Lys Gly Asp
```

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```
Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe Pro Pro Asn
                                120
         115
Gly Pro Val Met Gln Arg Arg Ile Arg Gly Trp Glu Pro Ser Thr Glu
130 135 140
Val Met Tyr Val Asp Asp Lys Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
Asn Met Ala Leu Leu Leu Lys Asp Gly Arg His Leu Arg Val Asp Phe
165 170 175
                  165
             Tyr Ile Pro Lys Lys Lys Val Glu Asn Met Pro Asp Tyr 180 185 190
                                                            190
His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys
195 200 205
Pro Val Lys Leu Tyr Glu Cys Ala Val Ala Arg Tyr Ser Leu Leu Pro
210 215 220
Glu Lys Asn Lys Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu 225 230 235
Ser Thr Arg Thr Gly
<210> 159
<211> 588
<212> DNA
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                                                                                  60
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ggaaaccgta cattcaccaa atacccaaaa gagataccag actatttcaa gcagaccttt
                                                                                 180
cctgaaggct atcactggga gcgaagcatt ccttttcaag accaggcctc atgtaccgtc
acaagcgaca tcagtgtgaa aggtgactct ttcttctatg acattaagtt cactggcatg aactttcctc ctcatggtcc agtgatgcag agaaagacag taaaatggga gccatccact
                                                                                 240
                                                                                 300
gaacgattgt atcttcgcga cggtgtgctg acgggagata tccacaagac tctgaaactt
                                                                                 360
                                                                                 420
āgcgģtggēg gccattācāc atgtģtētētt aaāāctāttt acagatcēaa gcaētcgatc
aacatgccgg atttccattt tatagaccac cgcattgaga ttctgggcaa cccagaagac
aagccggtca agctgtacga gattgctaca gctcgccatc atgggctgaa gggtaagcct
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                                                                                 588
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<211> 196
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                                         10
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Pro Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg
Ser Ile Pro Phe Gln Asp Gln Ala Ser Cys Thr Val Thr Ser Asp Ile
    Val Lys Gly Asp Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met
Asn Phe Pro Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp
85 90 95
Glu Pro Ser Thr Glu Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly
                                     105
Asp Ile His Lys Thr Leu Lys Leu Ser Gly Gly Gly His Tyr Thr Cys
                                            Page 78
```

```
Val Phe Lys Thr ITe Tyr Arg Ser Lys His Ser ITe Asn Met Pro Asp
130 140
 Phe His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp
Lys Pro Val Lys Leu Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu
165 170 175
Lys Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp
               180
                                        185
 Thr Gly Tyr
               Ser
 <210> 161
 <211> 738
 <212> DNA
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<223> Synthetically generated
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                                                                                       120
catcttacag agaaggaagg caagcctctg ccgttttctt tcgatatatt gacaccagca
tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag
                                                                                       180
                                                                                       240
cagacette etgaaggeta teactgggag egaaaaatga ettatgagga eggggeata agtaaegtee gaageeacat eaggatgaaa gaggaagagg ageggeattt etactataag atteaettea etggegagtt teeteeteat ggteeagtga tgeagagaaa gaeagtaaaa
                                                                                       300
                                                                                       360
tgggagccat ccactgaaaa catttatcct cgcgacgaat ttctggaggg acatgacgac
                                                                                       480
atgactctgc gggttgaagg tggcggctat tacagagctg aatttagaag ttcttacaaa
                                                                                       540
ggcaagaaga aggtcgagaa tatgcctgac taccatttta tagaccaccg cattgagatt atggagcatg acgaggacta caaccatgtc aagctgcgcg agtgtgctgt agctcgctat
                                                                                       600
                                                                                       660
tcictgctgc ctgagaagaa caagggtaag cciatcccta accctctcct cggacicgat
                                                                                       720
tctacgcgta ccggttag
                                                                                       738
<210> 162
<211> 245
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<213> Artificial Sequence
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<223> Synthetically generated
<400> 162
Met Lys Gly Val Lys Glu Val Met Lys Ile Ser Leu Glu Met Asp Cys

10
15
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Pro Tyr Ala Gly Thr Gln Thr Leu His Leu Thr Glu Lys Glu Gly Lys
35 40 . 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
GÎn Thr Phe Pro Glu GÎy Tyr His Trp Glu Arg Lys Met Thr Tyr Glu
85 90 95
Asp Gly Gly Ile Ser Asn Val Arg Ser His Ile Arg Met Lys Glu Glu 100 105 110
Glu Glu Arg His Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro
115 120 125
Pro His Gly Pro Val Met Glm Arg Lys Thr Val Lys Trp Glu Pro Ser
                             135
Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly His Asp Asp
```

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```
Met Thr Leu Arg Val Glu Gly Gly Gly Tyr Tyr Arg Ala Glu Phe Arg
165 170 175
Ser Ser Tyr Lys Gly Lys Lys Lys Val Glu Asn Met Pro Asp Tyr His
Phe Ile Asp His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn
195 200 205
    Val Lys Leu Arg Glu Cys Ala Val Ala Arg Tyr Ser Leu Leu Pro
210 215 220
Glu Lys Asn Lys Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp
225 230 235 240
Ser Thr Arg Thr Gly
<210> 163
<211> 603
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
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ggaaacaagt cattcgtcag ctacccaaaa gagataccag actatttcaa gcagaccttt
                                                                                         120
cctgaaggct atcactggga gcgaataatg acttttgagg acgggggcgt atgttgcatc
acaagcgaca tcagtatgaa aagtaacaac tgtttcttct atgacattaa gttcactggc
                                                                                         180
                                                                                         240
atgaactttc ctcctaatgg tccagtgatg cagaggagga tacgaggatg ggagccatcc
                                                                                         300
actgaacgat tgtatcttcg cgacggtgtg ctgacgggag atgtcaacat ggctctgttg
                                                                                         360
cttaaagatg gcggctatta cagagctgaa tttagaagtt cttacaaagg caagaagaac ctcacgcttc cggattgctt ctattatgta gacaccaaac ttgagattct gggcaaccca gaagacaagc cggtcaagct gtacgagtgt gctgtagctc gctattctct gctgcctgag aagaacaagg gtaagcctat ccctaaccct ctcctcggac tcgattctac gcgtaccggt
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                                                                                         480
                                                                                         540
                                                                                         600
                                                                                         603
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<211> 200
<212> PRT
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<220>
<223> Synthetically generated
<400> 164
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1 10 15
                                             10
Gln Leu Gln Tyr Gly Asn Lys Ser Phe Val Ser Tyr Pro Lys Glu Ile
20 _ _ _ _ 25 _ _ 30 _
Pro Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg
Ile Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile 50 55 60
Ser Met Lys Ser Asn Asn Cys Phe Phe Tyr Asp Ile Lys Phe Thr Gly 75 80
Met Asn Phe Pro Pro Asn Gly Pro Val Met Gln Arg Arg Ile Arg Gly
Trp Glu Pro Ser Thr Glu Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr
100 105 110
Gly Asp Val Asn Met Ala Leu Leu Leu Lys Asp Gly Gly Tyr Tyr Arg
115 120 125
                                   120
Ala Glu Phe Arg Ser Ser Tyr Lys Gly Lys Lys Asn Leu Thr Leu Pro
130 135 140
Asp Cys Phe Tyr Tyr Val Asp Thr Lys Leu Glu Ile Leu Gly Asn Pro
145 150 155 160
Glu Asp Lys Pro Val Lys Leu Tyr Glu Cys Ala Val Ala Arg Tyr Ser
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Leu Leu Pro Glu Lys Asn Lys Gly Lys Pro Ile Pro Asn Pro Leu Leu
 Gly Leu Asp Ser Thr Arg Thr Gly
 <210> 165
 <211> 663
 <212> DNA
 <213> Artificial Sequence
 <223> Synthetically generated
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gacaaatttg agatcgaagg ggagggaaac ggaaaacctt acgcaggaac acagactta
                                                                                       120
catcttacag agaaggaagg caagcctctg ccgtttggtt ggcatatatt gtcaccagca tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag cagacctttc ctgaaggcta tcactgggag cgaagcattc cttttcaaga ccaggctca
                                                                                       180
                                                                                       240
                                                                                       300
tgtaccgtca caagcgacat cagtatgaaa agtaacaact gtttcttcta tgacattaag
                                                                                       360
ttcactggca tgaactttcc tcctcatggt ccagtgatgc agagaaagac agtaaaatgg gagccatca ctgaaaacat ttatcctcgc gacgaatttc tggagggaga tgtcaacatg gctctgttgc ttaaagatgg cggccattac acatgtgtct ttaaaactat ttacagatcc
                                                                                       420
                                                                                       480
                                                                                       540
aagcačtoga tcaacatgčč ggatttccat tttaťagacc accgcattga tattcggaag
                                                                                       600
ttcgacgaaa attacatcaa cgcgagcagg acgagattgc tacagctcgc catcatgggc
                                                                                       660
                                                                                       663
<210> 166
<211> 220
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
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1 10 15
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Pro Tyr Ala Gly Thr Gln Thr Leu His Leu Thr Glu Lys Glu Gly Lys
Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Ala Phe Met Tyr Gly 50 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gin Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Ile Pro Phe Gln
85 90 95
Asp Gln Ala Ser Cys Thr Val Thr Ser Asp Ile Ser Met Lys Ser Asn 100 105 110
Asn Cys Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe Pro Pro 115 120 125
His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr
Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val Asn Met
145 150 155 160
Ala Leu Leu Lys Asp Gly Gly His Tyr Thr Cys Val Phe Lys Thr
165 170 175
Ile Tyr Arg Ser Lys His Ser Ile Asn Met Pro Asp Phe His Phe Ile
                                       185
              Ile Asp Ile Arg Lys Phe Asp Glu Asn Tyr Ile Asn Ala
Ser Arg Thr Arg Leu Leu Gln Leu Ala Ile Met Gly
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 <211> 726
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetically generated
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 caccactita cgatcaaagg ggaaggagga ggataccctt acgaaggagt acagtttatg
                                                                                       120
tctcttgaag tggtgaatgg cgcgcctctg ccgttttctt tcgatatatt gacaccagca tttcagtatg gaaaccgtac attcaccaaa tacccaaaag agataccaga ctatttcaag cagacctttc ctgaaggcta tcactgggag cgaataatga cttttgagga cgggggcgta
                                                                                       180
                                                                                       240
                                                                                       300
 tgttgcatca caagccacat caggatgaaa gaggaagagg agcggcattt ctactataag
                                                                                       360
attcacttca ctggcgagtt tcctcctcat ggtccagtga tgcagagaaa gacagtaaaa
                                                                                       420
tgggagccat ccactgaaaa catttatcct cgcgacgaat ttctggaggg agatgtcaac atggctctgt tgcttaaaga tggcggccat tacacatgtg tctttaaaac tatttacaga tccaagaaga aggtcgagaa tatgcctgac taccattta tagaccaccg cattgagatt
                                                                                       480
                                                                                       540
                                                                                       600
atggagcatg acgaggacta caaccatgtc aagctgcgcg agattgctac agctcgccat
                                                                                       660
catgggctga agggtaagcc tatccctaac cctctcctcg gactcgattc tacgcgtacc
                                                                                       720
ggttag
                                                                                       726
<210> 168
<211> 241
 <212> PRT
 <213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 168
Met Lys Gly Val Lys Glu Val Met Lys Ile Ser Leu Glu Met Glu Gly

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15
Ala Val Asn Gly His His Phe Thr Ile Lys Gly Glu Gly Gly Tyr
Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala 35 40 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Gln Tyr Gly 50 _ _ 60
Asn Arg Thr Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys
65 70 75 80
Gin Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
85 90 95
Asp Gly Gly Val Cys Cys Ile Thr Ser His Ile Arg Met Lys Glu Glu
100 105 110
Glu Glu Arg His Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro
Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser
Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val Asn 145 150 155 160
Met Ala Leu Leu Lys Asp Gly Gly His Tyr Thr Cys Val Phe Lys
                   165
                                            170
Thr Ile Tyr Arg Ser Lys Lys Lys Val Glu Asn Met Pro Asp Tyr His
180
185
190
Phe Ile Asp His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn
                                  200
His Val Lys Leu Arg Glu Ile Ala Thr Ala Arg His His Gly Leu Lys 210 220
Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg 225 235
                                               Page 82
```

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<210> 169
<211> 624
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
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                                                                                              120
                                                                                              180
ttcgatatat tgacaccagc atttatgtat ggaaaccgtg tattcaccaa atacccaaaa
gagataccag actatttcaa gcagaccttt cctgaaggct atcactggga gcgaataatg acttttgagg acggggggt atgttgcatc acaagcgaca tcagtgtgaa aggtgactct ttcttctatg acattaagtt cactggcatg aactttcctc ctcatggtcc agtgatgcag
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                                                                                              300
                                                                                              360
agaaagacag taaaatggga gccatccact gaaaacattt atcctcgcga cgaatttctg gagggagatg tcaacatggc tctgttgctt aaagatggcg gccattacac atgtgtcttt aaaaactattt acagatccaa gcactcgatc aacatgccgg atttccattt tatagaccac cgcattgaga ttatggagca tgacgaggac tacaaccatg tcaagctgcg cgagattgct
                                                                                              420
                                                                                              480
                                                                                              540
                                                                                              600
acagetegee atcatggget gaag
                                                                                              624
<210> 170
<211> 208
<212> PRT
<213> Artificial Sequence
<223> Synthetically generated
<400> 170
Met Glu Gly Ala Val Asn Gly His His Phe Glu Ile Glu Gly Glu Gly
Asn Gly Lys Pro Tyr Ala Gly Val Gln Phe Met Ser Leu Glu Val Val 20 25 30
Asn Gly Ala Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe 35 45
Met Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp 50 60
Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met 65 70 75 80
Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val
85 90 95
Lys Gly Asp Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe 100 105 110
Pro Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro
115 120 125
                                     120
    Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val
     130
                                135
Asn Met Ala Leu Leu Leu Lys Asp Gly Gly His Tyr Thr Cys Val Phe 145 150 155 160
Lys Thr Ile Tyr Arg Ser Lys His Ser Ile Asn Met Pro Asp Phe His 175
Phe Ile Asp His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn
180 185 190
His Val Lys Leu Arg Glu Ile Ala Thr Ala Arg His His Gly Leu Lys
195 200 205
<210> 171
<211> 702
<212> DNA
<213> Artificial Sequence
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<220>
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gaaggaggag gataccetta cgaaggaaca aattttgtaa aacttgtagt gacgaaaggc
gggcetetge egtttggttg geatatattg teaceacaat tacagtatgg aaacaagtea
                                                                              120
                                                                              180
řťčgtcagčt ačccagčcgá ťataccagač tatatcaagc tgtcčtttčc tgagggcttt
                                                                              240
300
                                                                              360
                                                                              420
                                                                              480
                                                                              540
ggcggccatt acacatgtgt ctttaaaact atttacagat ccaagaagaa cctcacgctt
                                                                              600
ccggattgct tctattatgt agacaccaaa cttgagattc tgggcaaccc agaagacaag
ccggtcaagc tgtacgagat tgctacagct cgccatcatg ggctgaaggg taagcctatcctaaccctc tcctcggact cgattctacg cgtaccggtt ag
                                                                              660
                                                                              702
<210> 172
<211> 233
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
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Thr Ile Lys Gly Gly Gly Gly Tyr Pro Tyr Glu Gly Thr Asn Phe
20 25 30
Val Lys Leu Val Val Thr Lys Gly Gly Pro Leu Pro Phe Gly Trp His
35 40 45
Ile Leu Ser Pro Gln Leu Gln Tyr Gly Asn Lys Ser Phe Val Ser Tyr 50 60
Pro Ala Asp Ile Pro Asp Tyr Ile Lys Leu Ser Phe Pro Glu Gly Phe 65 70 75 80
Thr Trp Glu Arg Lys Met Thr Tyr Glu Asp Gly Gly Ile Ser Asn Val
85 90 95
Arg Ser His Ile Arg Met Lys Glu Glu Glu Arg His Phe Tyr Tyr
    The His Phe Thr Gly Glu Phe Pro Pro His Gly Pro Val Met Gln 115 120 125
         115
                               120
    Lys Thr Val Lys Trp Glu Pro Ser Thr Glu Asn Ile Tyr Pro Arg
                           135
Asp Glu Phe Leu Glu Gly His Asp Asp Met Thr Leu Arg Val Glu Gly 145
Gly Gly His Tyr Thr Cys Val Phe Lys Thr Ile Tyr Arg Ser Lys Lys
165 170 175
                  165
                                        170
Asn Leu Thr Leu Pro Asp Cys Phe Tyr Tyr Val Asp Thr Lys Leu Glu
180 185 190
Ile Leu Gly Asn Pro Glu Asp Lys Pro Val Lys Leu Tyr Glu Ile Ala
195 200 205
Thr Ala Arg His His Gly Leu Lys Gly Lys Pro Ile Pro Asn Pro Leu 210 220
Leu Gly Leu Asp Ser Thr Arg Thr Gly
<210> 173
<211> 729
<212> DNA
<213> Artificial Sequence
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tctcttgaag tggtgaatgg cgcgcctctg ccgttttctt tcgatatatt gacaccagca
 tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag
 cagacctttc ctgaaggcta tcactgggag cgaaaaatga cttatgagga cgggggcata
agtaacgtcc gaagcgacat cagtgtgaaa ggtgactctt tctactataa gattcacttc actggcgagt ttcctcctaa tggtccagtg atgcagagga ggatacgagg atgggagcca tccactgaaa acatttatcc tcgcgacgaa tttctggagg gacatgacga catgactctg cgggttgaag gtggccgcca tttggaggtt gactttaaca ctcttacat acccaagaag
 aaggtcgaga atatgcctga ctaccatttt atagaccacc gcattgagat tatggagcat
 gacgaggact acaaccatgt caagctgcgc gagtgtgctg tagctcgcta ttctctgctgcctgagaaga acaagggtaa gcctatccct aaccctctcc tcggactcga ttctacgcgt
 accggttag
<210> 174
<211> 242
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetically generated
<400> 174
Met Lys Gly Val Lys Glu Val Met Lys Ile Ser Leu Glu Met Asp Cys
10 15
                                               10
Thr Val Asn Gly Asp Lys Phe Thr Ile Lys Gly Glu Gly Gly Tyr
Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala 35 40 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
GÎn Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Lys Met Thr Tyr Glu
85 90 95
Asp Gly Gly Ile Ser Asn Val Arg Ser Asp Ile Ser Val Lys Gly Asp
100 105 110
Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Asn Gly
115 120 125
Pro Val Met Gln Arg Arg Ile Arg Gly Trp Glu Pro Ser Thr Glu Asn 130 135
Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly His Asp Asp Met Thr Leu
                                                    155
Arg Val Glu Gly Gly Arg His Leu Arg Val Asp Phe Asn Thr Ser Tyr
165 170 175
                                               170
Ile Pro Lys Lys Val Glu Asn Met Pro Asp Tyr His Phe Ile Asp
180
185
190
His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn His Val Lys
195 200 205
Leu Arg Glu Cys Ala Val Ala Arg Tyr Ser Leu Leu Pro Glu Lys Asn 210 220
Lys Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg
225 230 235 240
Thr Gly
<210> 175
<211> 663
<212> DNA
<213> Artificial Sequence
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120 180

240

300

600

660 720

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<220>
 <223> Synthetically generated
 <400> 175
atgaaggggg tgaaggaagt aatgaagatc agtctggaga tggactgcac tgttaacggc
gacaaattta cgatcaaagg ggaaggagga ggataccctt acgaaggaac acagacttta catcttacag agaaggaagg caagcctctg ccgtttggtt ggcatatatt gtcaccagca
tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag
cagacctttc ctgaaggcta tcactgggag cgaataatga cttttgagga cgggggcgta
tgttgcatca caagcgacat cagtgtgaaa ggtgactctt tctactataa gattcacttc actggcgagt ttcctcctca tggtccagtg atgcagagaa agacagtaaa atgggagcca tccactgaaa acatttatcc tcgcgacgaa tttctggagg gagatgtcaa catggctctg ttgcttaaaag atggcggcca ttacacatgt gtctttaaaa ctatttacag atccaagaag
aaggtcgaga atatgcctga ctaccatttt atagaccacc gcattgagat tatggagcat
gacgaggact acaaccatgt caagctgcgc gagattgcta cagctcgcca tcatgggctg
tag
<210> 176
<211> 220
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 176
Met Lys Gly Val Lys Glu Val Met Lys Ile Ser Leu Glu Met Asp Cys
1 10 15
Thr Val Asn Gly Asp Lys Phe Thr Ile Lys Gly Glu Gly Gly Tyr
Pro Tyr Glu Gly Thr Gln Thr Leu His Leu Thr Glu Lys Glu Gly Lys 35 40 45
Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Ala Phe Met Tyr Gly
                              55
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
85 90 95
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp
100 105 110
Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His Gly
Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu Asn 130 140
Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val Asn Met Ala Leu 145 150 160
Leu Leu Lys Asp Gly Gly His Tyr Thr Cys Val Phe Lys Thr Ile Tyr
165 170 175
Arg Ser Lys Lys Lys Val Glu Asn Met Pro Asp Tyr His Phe Ile Asp
                                        185
His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn His Val Lys
                                  200
Leu Arg Glu Ile Ala Thr Ala Arg His His Gly Leu
210 215 220
<210> 177
<211> 726
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 177
```

120 180

240

300

600

660

```
atgaaggggg tgaaggaagt aatgaagatc agtctggaga tggactgcac tgttaacggc
gacaaattta cgatcaaagg ggaaggagga ggataccctt acgaaggagt acagtttatg
tctcttgaag tggtgaatgg cgcgcctctg ccgtttggtt ggcatatait gtcaccagca
tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag cagacctttc ctgaaggcta tcactgggag cgaaaaatga cttatgagga cgggggcata agtaacgtcc gaagcgacat cagtgtgaaa ggtgactctt tctactataa gattcacttc actggcgagt ttcctctca tggtccagtg atgcagagaa agacagtaaa atgggagcca
tccactgaag taatgtatgt tgacgacaag agtgacggtg tgctgaaggg agatgtcaac
atggctčtgť tgctťaaaga tggcggccať tácácaťgťg tčttťaaáác táttťacaga
tccaagaaga aggtcgagaa tatgcctgac taccatttta tagaccaccg cattgagatt atggagcatg acgaggacta caaccatgtc aagctgcgcg agattgctac agctcgccat
catgggctga agggtaagcc tatccctaac cctctcctcg gactcgattc tacgcgtacc
ggttag
<210> 178
<211> 241
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 178
Met Lys Gly Val Lys Glu Val Met Lys Ile Ser Leu Glu Met Asp Cys
1 10 15
Thr Val Asn Gly Asp Lys Phe Thr Ile Lys Gly Glu Gly Gly Tyr 20 25 30
Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala
Pro Leu Pro Phe Gly Trp His Ile Leu Ser Pro Ala Phe Met Tyr Gly 50 55 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 75 75 80
GÎN Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Lys Met Thr Tyr Glu
85 90 95
Asp Gly Gly Ile Ser Asn Val Arg Ser Asp Ile Ser Val Lys Gly Asp 100 105 110
Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His Gly
115
120
125
Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu Val
130 135 140
Met Tyr Val Asp Asp Lys Ser Asp Gly Val Leu Lys Gly Asp Val Asn
145 150 155 160
Met Ala Leu Leu Leu Lys Asp Gly Gly His Tyr Thr Cys Val Phe Lys
165 170 175
Thr Ile Tyr Arg Ser Lys Lys Lys Val Glu Asn Met Pro Asp Tyr His
180 185 190
Phe Ile Asp His Arg Ile Glu Ile Met Glu His Asp Glu Asp Tyr Asn
195 200 205
His Val Lys Leu Arg Glu Ile Ala Thr Ala Arg His His Gly Leu Lys 210 220
Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr
225 230 235 240
Gly
<210> 179
<211> 825
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
```

120

180

540

600 660

```
<400> 179
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 actagtgctg attcgtcgaa ctcttactct ggatcctcct tcgcgaatgg gattgcggaa
 gaaatgatga ccgatctgca tctggactgc actgttaacg gcgacaaatt tacgatcaaa
ggggaaggag gaggataccc ttacgaagga gtacagttta tgtctcttga agtggtgaat
 ggcgcgcctc tgccgttttc tttcgatāta ītgacāccag cātttatgta tggādaccgt
 gtattcacca aătacccaaa agagătacca gactatttca agcagacctt tectgaaggc
 tatcactggg agcgaataat gacttttgag gacggggggg tatgttgcat cacaagcgac atcagtgtga aaggtgactc tttcttctat gacattaagt tcactggcat gacattct
 cctaatggtc cagtgatgca gaggaggata cgaggatggg agccatccac tgaacgattg
tatcttcgcg acggtgtgct gacgggacat gacgacatga ctctgcgggt tgaaggtggc
 cgccatttga gagttgactt taacacttct tacataccca agaagaacct cacgcttccg
 gattgcttct attatgtaga caccaaactt gatattcgga agttcgacga aaattacatc
 aacgicgagc aggacgagāt igciacagci cgccaicāig ggcigaaggg taagcciatc
 cctăacccic tcctcggact cgattctacg cgtaccggta gctcg
 <210> 180
<211> 275
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetically generated
 <400> 180
Met Met Ala Ile Ser Ala Leu Lys Asn Val Ile Ile Ile Val Ile Ile
Tyr Ser Cys Ser Thr Ser Ala Asp Ser Ser Asn Ser Tyr Ser Gly Ser
Ser Phe Ala Asn Gly Ile Ala Glu Glu Met Met Thr Asp Leu His Leu
35 40 45
Asp Cys Thr Val Asn Gly Asp Lys Phe Thr Ile Lys Gly Glu Gly Gly 50 60
Gly Tyr Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn
65 70 75 80
Gly Ala Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met
Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr
                                      105
Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr
115 120 125
Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys 130 140
Gly Asp Ser Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe Pro
145 150 155 160
Pro Asn Gly Pro Val Met Gln Arg Arg Ile Arg Gly Trp Glu Pro Ser
                   165
Thr Glu Arg Leu Tyr Leu Arg Asp Gly Val Leu Thr Gly His Asp Asp 180 185 190
Met Thr Leu Arg Val Glu Gly Gly Arg His Leu Arg Val Asp Phe Asn
195 200 205
    Ser Tyr Ile Pro Lys Lys Asn Leu Thr Leu Pro Asp Cys Phe Tyr 210 220
Tyr Val Asp Thr Lys Leu Asp Ile Arg Lys Phe Asp Glu Asn Tyr Ile
225 230 235 240
Asn Val Glu Gln Asp Glu Ile Ala Thr Ala Arg His His Gly Leu Lys 250 255
Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr 260 265 270
Gly Ser Ser
275
<210> 181
<211> 750
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120

180 240

300

360

420 480

540 600

660

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<212> DNA
<213> Artificial Sequence
<223> Synthetically generated
<400> 181
                                                                                 60
atgagtcatt ccaagagtgt gatcaaggac gaaatgttca tcaagattca tctggaaggc
acttttaacg gccacaaatt tacgatcaaa ggggaaggag gaggataccc ttacgaagga
                                                                                120
                                                                                180
gtacagttta tgtctcttga agtggtgaat ggcgcgcctc tgccgttttc tttcgatata
ttgacaccag catttatgta tggaaaccgt gtattcacca aatacccaaa agagatacca gactatttca agcagacctt tcctgaaggc tatcactggg agcgaataat gacttttgag
                                                                                240
                                                                                300
gacgggggcg tatgitgcat cacaagccac atcaggaiga aagaggaaga ggagcggcai
                                                                                360
                                                                                420
ttcttctatg acattaagtt cactggcatg aactttcctc ctcatggtcc agtgatgcag
agaaagacag taaaatggga gccatccact gaacgattgt atcttcgcga cggtgtgctg
                                                                                480
acgggacatg acgacatgac tctgcgggtt gaaggtggcc gccatttgag agttgacttt aacacttctt acatacccaa gcactcgatc aacatgccgg atttccattt tatagaccac
                                                                                540
                                                                                600
cgcattgaga ttatggagca tgacgaggac tacaaccatg tcaagctgcg cgagtgtgct
                                                                                660
gtagctcgct attctctgct gcctgagaag aacaagggta agcctatccc taaccctctc
                                                                                720
                                                                                750
ctcggactcg attctacgcg taccggttag
<210> 182
<211> 249
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
Met Ser His Ser Lys Ser Val Ile Lys Asp Glu Met Phe Ile Lys Ile
1 10 15
His Leu Glu Gly Thr Phe Asn Gly His Lys Phe Thr Ile Lys Gly Glu
20 25 30
Gly Gly Tyr Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val
35 40 45
    Asn Gly Ala Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala 50 55 60
Phe Met Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro 65 70 75 80
Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Île
85 90 95
Met Thr Phe Glu Asp Gly Gly Val Cys Cys Ile Thr Ser His Ile Arg
100 105 110
Met Lys Glu Glu Glu Arg His Phe Phe Tyr Asp Ile Lys Phe Thr
                                120
Gly Met Asn Phe Pro Pro His Gly Pro Val Met Gln Arg Lys Thr Val
                           135
    Trp Glu Pro Ser Thr Glu Arg Leu Tyr Leu Arg Asp Gly Val Leu
Thr Gly His Asp Asp Met Thr Leu Arg Val Glu Gly Gly Arg His Leu
165 170 175
Arg Val Asp Phe Asn Thr Ser Tyr Ile Pro Lys His Ser Ile Asn Met
    Asp Phe His Phe Ile Asp His Arg Ile Glu Ile Met Glu His Asp
         195
                                200
        Tyr Asn His Val Lys Leu Arg Glu Cys Ala Val Ala Arg Tyr
215 220
Ser Leu Leu Pro Glu Lys Asn Lys Gly Lys Pro Île Pro Asn Pro
225 230 235
Leu Gly Leu Asp Ser Thr Arg Thr Gly 245
```

```
<211> 726
<212> DNA
<213> Artificial Sequence
<223> Synthetically generated
<400> 183
atgaaggggg tgaaggaagt aatgaagatc agtctggaga tggactgcac tgttaacggc
                                                                                  60
gacaaattta cgatcaaagg ggaaggagga ggataccctt acgaaggaac aaattttgta
                                                                                 120
aaacttgtag tgacgaaagg cgggcctctg ccgttttctt tcgatatatt gacaccagca
                                                                                 180
tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag cagacctttc ctgaaggcta tcactgggag cgaataatga cttttgagga cgggggcgta
                                                                                 240
                                                                                 300
tgttgcatca caagcgacat cagtgtgaaa ggtgactctt tcttctatga cattaagttc
                                                                                 360
actggcatga actiticetce teatggicea gigatgeaga gaaagacagt aaaatgggag
                                                                                 420
ccatccactg aagtaatgta tgttgacgac aagagtgacg gtgtgctgāa gggagātgtc
                                                                                 480
aacatggctc tgttgcttaa agatggccgc catttgagag ttgactttaa cacttcttac atacccaaga agaaggtcga gaatatgcct gactaccatt ttatagacca ccgcattgag
                                                                                 540
                                                                                 600
attctgggča ačccagaaga čaagccggtc aagctgtacg agattgctac agčtcgcčať
                                                                                 660
catgggctga agggtaagcc tatccctaac cctctcctcg gactcgattc tacgcgtacc
                                                                                 720
ggttag
<210> 184
<211> 241
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 184
Met Lys Gly Val Lys Glu Val Met Lys Ile Ser Leu Glu Met Asp Cys
    Val Asn Gly Asp Lys Phe Thr Ile Lys Gly Glu Gly Gly Tyr
20 25 30
Pro Tyr Glu Gly Thr Asn Phe Val Lys Leu Val Val Thr Lys Gly Gly 35 40 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu
85 90 95
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp
   Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe Pro Pro His 115 120 125
Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu
130 135 140
Val Met Tyr Val Asp Asp Lys Ser Asp Gly Val Leu Lys Gly Asp Val
145 150 155 160
                                                                     160
Asn Met Ala Leu Leu Leu Lys Asp Gly Arg His Leu Arg Val Asp Phe
165 170 175
Asn Thr Ser Tyr Ile Pro Lys Lys Val Glu Asn Met Pro Asp Tyr
180 185 190
His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys
         195
                                200
                                                       205
Pro Val Lys Leu Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu Lys
                            215
                                                   220
Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg
225 230 235
Gly
```

```
<210> 185
<211> 726
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 185
atgaaggggg tgaaggaagt aatgaagatc agtctggaga tggactgcac tgttaacggc
                                                                                      60
gacaaattta cgatcaaagg ggaaggagga ggataccctt acgaaggaac acagacttta catcttacag agaaggaagg caagcctctg acgttttctt tcgatgtatt gacaccacaa
                                                                                     120
                                                                                     180
ttacagtatg gaaacaagtc attcgtcagc tacccaaaag agataccaga ctatttcaag
                                                                                     240
cagacettte etgaaggeta teaetgggag egaageatte etttteaaga ecaggeetea
                                                                                     300
tgtaccgtca caagccacat caggatgaaa gaggaagagg agcggcattt cttctatgacattaagttca ctggcatgaa ctttcctcct catggtccag tgatgcagag aaagacagta
                                                                                     360
                                                                                     420
aaatgggagc catccactga aaacatttat cctcgcgacg aatttctgga gggacatgac
                                                                                     480
gacatgactc tgcgggttga aggtggccgc catttgagag ttgactttaa cacttcttac
                                                                                     540
átaccčaaga agaaggtega gaatatgeet gactačeatt ttatagaeca cegeattgag attetgggea acceagaaga caageeggte aagetgtaeg agattgetae agetegeeat
                                                                                     600
                                                                                     660
catgggctga agggtaagcc tatccctaac actctcctcg gactcgattc tacgcgtacc
                                                                                     720
ggttag
                                                                                     726
<210> 186
<211> 241
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 186
Met Lys Gly Val Lys Glu Val Met Lys Ile Ser Leu Glu Met Asp Cys

1 10 15
Thr Val Asn Gly Asp Lys Phe Thr Ile Lys Gly Glu Gly Gly Gly Tyr
20 25 30
Pro Tyr Glu Gly Thr Gln Thr Leu His Leu Thr Glu Lys Glu Gly Lys
35 40 45
Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Gln Leu Gln Tyr Gly 50 60
Asn Lys Ser Phe Val Ser Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys
65 70 75 80
GÎN Thr Phe Pro Glu GÎy Tyr His Trp Glu Arg Ser Ile Pro Phe GÎN
85 90 95
Asp Gln Ala Ser Cys Thr Val Thr Ser His Ile Arg Met Lys Glu Glu
100 105 110
Glu Glu Arg His Phe Phe Tyr Asp Ile Lys Phe Thr Gly Met Asn Phe 115 120 125
Pro Pro His Gly Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro
                             135
     130
    Thr Glu Asn Ile Tyr Pro Arg Asp Glu Phe Leu Glu Gly His Asp
150 155 160
Asp Met Thr Leu Arg Val Glu Gly Gly Arg His Leu Arg Val Asp Phe
165 170 175
Asn Thr Ser Tyr Ile Pro Lys Lys Lys Val Glu Asn Met Pro Asp Tyr
180 185 190
His Phe Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys
         195
Pro Val Lys Leu Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu Lys
210 215 220
Gly Lys Pro Ile Pro Asn Thr Leu Leu Gly Leu Asp Ser Thr Arg
225 230 235
```

```
<210> 187
<211> 714
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 187
atgaaggggg tgaaggaagt aatgaagatc agtctggaga tggagggcgc tgttaacggc caccacttta cgatcaaagg ggaaggagga ggataccctt acgaaggaac acagacttta
                                                                                     60
                                                                                     120
catcttacag agaaggaagg čáagčctčťg ččgttttctt tcgatátatt gacáccagca
                                                                                     180
                                                                                     240
tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag
cagacctttc ctgaaggcta tcactgggag cgaataatga cttttgagga cgggggcgta
tgttgcatca caagcgacat cagtgtgaaa ggtgactctt tctactataa gattcacttc
                                                                                     300
                                                                                    360
actggcgagt ttcctcctca tggtccagtg atgcagagaa agacagtaaa atgggagcca
                                                                                    420
tccāctgaaa acatttatcc tcgcgacgaa tttctggagg gāgatgtcaa catggctctg
                                                                                    480
ttgcttaaag atggccgcca tttgagagtt gactttaaca cttcttacat acccaagaag
                                                                                    540
aaggtcgaga atatgcctga ctaccatttt atagaccacc gcattgagat tctgggcaac ccagaagaca agccggtcaa gctgtacgag attgctacag ctcgccatca tgggctgaag
                                                                                    600
                                                                                    660
ggtaagccta tccctaaccc tctcctcgga ctcgattcta cgcgtaccgg ttag
                                                                                    714
<210> 188
<211> 237
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 188
Met Lys Gly Val Lys Glu Val Met Lys Ile Ser Leu Glu Met Glu Gly
1 5 10 15
Ala Val Asn Gly His His Phe Thr Ile Lys Gly Glu Gly Gly Tyr
Pro Tyr Glu Gly Thr Gln Thr Leu His Leu Thr Glu Lys Glu Gly Lys
35 40 45
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr Gly 50 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ile Met Thr Phe Glu

85 90 95
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp
100 105 110
Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His Gly 115 120 125
Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu Asn
                             135
    Tyr Pro Arg Asp Glu Phe Leu Glu Gly Asp Val Asn Met Ala Leu
150 155 160
Leu Leu Lys Asp Gly Arg His Leu Arg Val Asp Phe Asn Thr Ser Tyr
165 170 175
Ile Pro Lys Lys Val Glu Asn Met Pro Asp Tyr His Phe Ile Asp
180 185 190
                                      185
His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val Lys Leu
Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly Lys Pro Ile
210 215 220
Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg
225 230 235
```

<210> 189

```
<211> 720
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 189
                                                                                   60
atgaaggggg tgaaggaagt aatgaagatc agtctggaga tggactgcac tgttaacggc
gačaaātītā cgatcāaagg ggaaggagga ggataccctt acgaaggagt acagtttātg
                                                                                  120
                                                                                  180
tctcttgaag tggtgaatgg cgcgcctctg acgttttctt tcgatgtatt gacaccagca
tttatgtatg gaaaccgtgt attcaccaaa tacccaaaag agataccaga ctatttcaag cagacctttc ctgaaggcta tcactgggag cgaataatga cttttgagga cgggggggta
                                                                                  240
                                                                                  300
tgitgcatca caagcgacat cagtgigaaa ggtgactcit tctaciaiaa gaiicacitc
                                                                                  360
                                                                                  420
ačtggcgagt ttcčtčctca tggtčcágtg átgčagagaa agacagtaaa átgggagcca
tccactgaag taatgtatgt tgacgacaag agtgacggtg tgctgaaggg agatgtcaac atggctctgt tgcttaaaga tggcggccat tacacatgtg tctttaaaac tatttacaga
                                                                                  480
                                                                                  540
                                                                                  600
tcčáagcačt cgatcaacát gččggátttc cattttaťag accaccgcat tgagattcťg
ggcaacccag aagacaagcc ggtcaagctg tacgagattg ctacagctcg ccatcatggg
                                                                                  660
                                                                                  720
ctgaagggta agcctatccc taaccctctc ctcggactcg attctacgcg taccggttag
<210> 190
<211> 239
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetically generated
<400> 190
Met Lys Gly Val Lys Glu Val Met Lys Ile Ser Leu Glu Met Asp Cys
1 5 10 15
Thr Val Asn Gly Asp Lys Phe Thr Ile Lys Gly Glu Gly Gly Gly Tyr 20 25 30
Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala
35 40 45
Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Ala Phe Met Tyr Gly 50 60
Asn Arg Val Phe Thr Lys Tyr Pro Lys Glu Ile Pro Asp Tyr Phe Lys 65 70 75 80
GIN Thr Phe Pro Glu GIy Tyr His Trp Glu Arg Ile Met Thr Phe Glu
85 90 95
Asp Gly Gly Val Cys Cys Ile Thr Ser Asp Ile Ser Val Lys Gly Asp
100 105 110
Ser Phe Tyr Tyr Lys Ile His Phe Thr Gly Glu Phe Pro Pro His Gly 115 120 125
Pro Val Met Gln Arg Lys Thr Val Lys Trp Glu Pro Ser Thr Glu Val
130 135 140
Met Tyr Val Asp Asp Lys Ser Asp Gly Val Leu Lys Gly Asp Val Asn
145 150 155 160
Met Ala Leu Leu Leu Lys Asp Gly Gly His Tyr Thr Cys Val Phe Lys
165 170 175
Thr Ile Tyr Arg Ser Lys His Ser Ile Asn Met Pro Asp Phe His Phe 180 185 190
Ile Asp His Arg Ile Glu Ile Leu Gly Asn Pro Glu Asp Lys Pro Val
195 200 205
         195
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Lys Leu Tyr Glu Ile Ala Thr Ala Arg His His Gly Leu Lys Gly Lys 210 220
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                                                                                       120
tatgttgácg acáagagíga öggtgtgctg áagggagátg tčaacatggc tötgťtgctť
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aaagatggcg gccattacac atgtgtcttt aaaactattt acagatccaa gcactcgatc
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aacatgccgg atttccattt tatagaccac cgcattgaga ttatggagca tgacgaggac tacaaccatg tcaagctgcg cgagattgct acagctcgcc atcatgggct gaagggtaag cctatcccta accetetect cggactcgat tctacgcgta ccggttag
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Trp Glu Pro Ser Thr Glu Val Met Tyr Val Asp Asp Lys Ser Asp Gly
    Leu Lys Gly Asp Val Asn Met Ala Leu Leu Leu Lys Asp Gly Gly 50 60
His Tyr Thr Cys Val Phe Lys Thr Ile Tyr Arg Ser Lys His Ser Ile 65 70 75 80
Asn Met Pro Asp Phe His Phe Ile Asp His Arg Ile Glu Ile Met Glu
85 90 95
His Asp Glu Asp Tyr Asn His Val Lys Leu Arg Glu Ile Ala Thr Ala
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Arg His His Gly Leu Lys Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly
115 120 125
Leu Asp Ser Thr Arg Thr Gly
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tttcagtatg gaaaccgtac attcaccaaa taccagccga tataccagac tatatcaagc tgtcctttcc tgagggcttt acctgggagc gaagcattcc ttttcaagac caggcctcat
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20 25 30
Pro Tyr Glu Gly Val Gln Phe Met Ser Leu Glu Val Val Asn Gly Ala
Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Gln Tyr Gly 50 60
    50
Asn Arg Thr Phe Thr Lys Tyr Gln Pro Ile Tyr Gln Thr Ile Ser 65 70 75
Cys Pro Phe Leu Arg Ala Leu Pro Gly Ser Glu Ala Phe Leu Phe Lys
85 90 95
Thr Arg Pro His Val Pro Ser Gln Ala Thr Ser Gly
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                                                                               120
                                                                               180
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                                                                               240
ctgtccttcc tgagggcttt acctgggagc gaagcattcc ttttcaagac caggcctcat
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Pro Tyr Glu Gly Thr Gln Thr Leu His Leu Thr Glu Lys Glu Gly Lys
35 40 45
Pro Leu Thr Phe Ser Phe Asp Val Leu Thr Pro Gln Leu Gln Tyr Gly 50 60
Asn Lys Ser Phe Val Ser Tyr Pro Ala Asp Ile Pro Asp Tyr Ile Lys
65 70 75 80
Leu Ser Phe Leu Arg Ala Leu Pro Gly Ser Glu Ala Phe Leu Phe Lys
85 90 95
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cgcgacggtg tgctgacggg acatgacgac atgactctgc gggttgaagg tggccgccat 180
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